

Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
			ID NO: 6049.		
1620	AAB94885	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16106.	1344	94
1620	gi19483920	Mus musculus	RIKEN cDNA 2310008M20 gene	1128	78
1620	AAG01968	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 6049.	534	83
1621	gi18676682	Homo sapiens	FLJ00240 protein	776	45
1621	gi14701866	Dictyostelium discoideum	carmil	314	22
1621	gi1881738	Acanthamoeba castellanii	myosin-I binding protein Acan125	305	26
1622	ABB07410	Homo sapiens	CYTO- Human kinesin motor protein, HsKip3A.	2108	98
1622	ABB07412	Homo sapiens	CYTO- Amino acid sequence of Kip3A fragment used in ATPase assay.	1796	96
1622	ABB07411	Homo sapiens	CYTO- Human HsKip3A motor domain fragment.	1723	98
1623	gi2887497	Homo sapiens	R34001_1	5418	100
1623	gi6069583	Mus musculus	JNK-binding protein JNKBP1	2339	47
1623	gi21430146	Drosophila melanogaster	LD01189p	1761	43
1624	gi17976802	Mus musculus	WD repeat domain 11 protein	770	59
1624	AAB73697	Homo sapiens	BIOR- Human bromodomain-containing protein 95.	769	59
1624	gi14286226	Homo sapiens	pleckstrin homology domain interacting protein	769	59
1625	gi11558488	Homo sapiens	B-cell lymphoma/leukaemia 11B	4438	100
1625	AAB99340	Homo sapiens	MOCH Human Rit1 beta protein sequence.	4434	99
1625	gi13094147	Mus musculus	zinc finger protein mRit1 beta	4063	93
1626	AAU03596	Homo sapiens	HOSP- Human 140kDa Shc associated protein (SAP140).	5366	93
1626	gi20381088	Homo sapiens	Similar to tudor repeat associator with PCTAIRE 2	5362	93
1626	gi5689375	Rattus norvegicus	tudor repeat associator with PCTAIRE 2	4545	77
1627	AAG03904	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 7985.	469	100
1627	gi2708307	Homo sapiens	U4/U6 small nuclear ribonucleoprotein hPrp3	469	100
1627	gi2853287	Homo sapiens	U4/U6-associated RNA splicing factor	469	100
1628	gi11611734	Homo sapiens	GREB1a	1504	46
1628	gi7264653	Mus musculus	Kiaa0575	1477	45
1628	gi11611736	Homo sapiens	GREB1b	1047	49
1629	AAAY94673	Homo sapiens	ZYMO Human zsig83 protein sequence.	948	100
1629	AAAY94674	Homo sapiens	ZYMO Human zsig83 mature protein sequence.	876	100
1629	AAB60475	Homo sapiens	INCY- Human cell cycle and proliferation protein CCYPR-23, SEQ ID NO:23.	196	43
1630	AAM93931	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 4104.	1326	96
1630	AAM93778	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3790.	1326	96

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SEQ ID	Hit ID	Species	Description	S score	Percent identity
1630	AAM93429	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3058.	1326	96
1631	AAM93943	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 4128.	2247	90
1631	gi12483904	Rattus norvegicus	zinc finger protein HIT-39	2083	83
1631	AAB21006	Homo sapiens	INCY- Human nucleic acid-binding protein, NuABP-10.	802	42
1632	AAB24467	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 31 SEQ ID NO:92.	289	32
1632	AAM83227	Homo sapiens	HUMA- Human immune/haematopoietic antigen SEQ ID NO:10820.	86	53
1632	gi 20886225 ref XP_123361.1	Mus musculus	similar to expressed sequence R74613	273	30
1633	AAW68581	Homo sapiens	INCY- Human COP9 protein.	956	90
1633	gi13111847	Homo sapiens	COP9 homolog	956	90
1633	gi1730284	Homo sapiens	COP9 signalosome subunit 1 CSN1	956	90
1634	AAB94678	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15628.	1526	100
1634	gi18490973	Mus musculus	RIKEN cDNA 1300006G11 gene	799	86
1634	AAU74448	Homo sapiens	OULU- Human protein sequence of lysyl hydroxylase 1 (LH1).	136	30
1635	gi18044855	Mus musculus	Similar to junction-mediating and regulatory protein	1425	82
1635	gi6573115	Mus musculus	p300 transcriptional cofactor JMY	1422	82
1635	gi8490223	Mus sp.	class V POU transcription factor	126	27
1636	gi1747	Oryctolagus cuniculus	trichohyalin	141	21
1636	gi3449364	Homo sapiens	intracellular hyaluronic acid binding protein; IHABP	141	25
1636	AAS17496_aa1	Homo sapiens	CANG- Human cDNA encoding a hyaluronic acid binding protein RHAMM.	140	25
1637	gi16356685	Homo sapiens	T-box transcription factor TBX22	2145	100
1637	gi10834638	Homo sapiens	TBXX T-box containing protein	2145	100
1637	gi4490920	Homo sapiens	dJ795G23.1 (T-Box family protein)	891	100
1638	gi12314237	Homo sapiens	bA127L20.4 (novel protein)	477	100
1638	gi4468665	Phoronis vancouverensis	cytoplasmic intermediate filament protein	113	25
1638	gi6682319	Mytilus galloprovincialis	myosin heavy chain	111	26
1639	gi12005487	Homo sapiens	NPD012	228	32
1639	AAB95811	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18804.	198	32
1639	gi18447198	Drosophila melanogaster	GH09355p	183	20
1640	AAB72699	Homo sapiens	UYWA- Human beta-globin gene repressor BP1.	1285	100
1640	gi19849183	Homo sapiens	distal-less homeo box 7	1285	100
1640	gi11141507	Homo sapiens	beta protein 1 BP1	1285	100
1641	gi4056437	Arabidopsis thaliana	Strong similarity to PFAM PF00069 Eukaryotic protein kinase domain.	79	40

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1641	gi8778584	Arabidopsis thaliana	F28C11.17	79	40
1641	gi4583513	Chrysomya bezziana	peritrophin-48 precursor	75	26
1642	gi1663698	Homo sapiens	expressed ubiquitously~product similar to D.melanogaster mam protein.	316	30
1642	gi6979930	Homo sapiens	Mam1	316	30
1642	gi11127697	Homo sapiens	SYT/SSX4v fusion protein	147	27
1643	gi1230657	Saccharomyces cerevisiae	Ssd1p	73	31
1643	gi172697	Saccharomyces cerevisiae	SRK1	73	31
1643	gi172612	Saccharomyces cerevisiae	SSD1 protein	73	31
1644	gi3298472	Mus musculus	zinc finger protein	2661	87
1644	gi14329524	Homo sapiens	dJ871E2.1 (novel protein (ortholog of mouse zinc finger protein Zan75))	1605	100
1644	gi5931618	Mus musculus	A kinase anchor protein 95	446	28
1645	gi15284214	Homo sapiens	double homeobox protein	264	42
1645	gi841206	Homo sapiens	homeobox sequence similar to that found in D4Z4 repeat, GenBank Accession Number L32607.	259	43
1645	gi1435038	Homo sapiens	facioscapulohumeral muscular dystrophy	257	42
1646	AAE02058	Homo sapiens	HUMA- Human four disulfide core domain (FDCD)-containing protein.	596	43
1646	AAM79986	Homo sapiens	HYSE- Human protein SEQ ID NO 3632.	587	38
1646	AAM79002	Homo sapiens	HYSE- Human protein SEQ ID NO 1664.	586	38
1647	gi19263709	Homo sapiens	Similar to LOC147700	989	100
1647	gi17939383	Homo sapiens	kinesin light chain	799	100
1647	gi10281106	Rattus norvegicus	kinesin light chain KLCT	743	90
1648	AAV59712	Homo sapiens	GEST Secreted protein 33-54-1-B9-FL1.	562	98
1648	gi3288566	Oryzias latipes	annexin max1	76	31
1648	gi6468754	Rattus norvegicus	SECIS binding protein 2	74	25
1649	gi28971	Homo sapiens	autoantigen NOR-90	741	43
1649	AAM69182	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 29488.	713	97
1649	AAM56802	Homo sapiens	MOLE- Human brain expressed single exon probe encoded protein SEQ ID NO: 28907.	713	97
1650	AAB43919	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:1364.	99	36
1650	gi214042	Xenopus laevis	alpha-1 type II collagen	88	30
1650	gi21105299	Mytilus galloprovincialis	precollagen-NG	85	29
1651	AAM93382	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 2963.	1762	100
1651	gi488555	Homo sapiens	zinc finger protein ZNF135	400	40
1651	AAM68363	Homo sapiens	MOLE- Human bone marrow	387	38

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			expressed probe encoded protein SEQ ID NO: 28669.		
1652	AAB95733	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18617.	3217	100
1652	AAB95128	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17131.	3217	100
1652	AAM79739	Homo sapiens	HYSE- Human protein SEQ ID NO 3385.	2361	50
1653	gi4092859	Homo sapiens	p53 regulated PA26-T2 nuclear protein	940	55
1653	gi4092863	Homo sapiens	non-p53 regulated PA26-T1 nuclear protein	938	56
1653	gi13161393	Xenopus laevis	nuclear factor XPA26-T2	905	53
1654	AAM39432	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2577.	3458	100
1654	gi15215576	Mus musculus	BMP-2 inducible kinase	2580	76
1654	AAM41218	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 6149.	2396	99
1655	gi11493485	Homo sapiens	PRO2574	384	100
1655	AAW73401	Homo sapiens	HUMA- Human secreted protein encoded by Gene No. 5.	71	36
1655	AAO10782	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 24674.	66	37
1656	gi13359303	Homo sapiens	MAGE-E1a	2593	99
1656	gi14588553	Homo sapiens	MAGE E1a	2593	99
1656	gi17974508	Homo sapiens	MAGED4 protein	2589	99
1657	gi11493552	Homo sapiens	PRO1933	661	100
1658	AAM89182	Homo sapiens	HUMA- Human immune/haematopoietic antigen SEQ ID NO:16775.	1972	98
1658	ABB04152	Homo sapiens	GENP- Immune response modulating protein TGAP7-beta.	908	43
1658	ABB04151	Homo sapiens	GENP- Immune response modulating protein TGAP7-alpha.	908	43
1659	gi577221	Saccharomyces cerevisiae	Imh1p	89	24
1659	gi21070617	Dictyostelium discoideum	HYPOTHETICAL 144.9 KDA PROTEIN	84	26
1659	ABB89609	Homo sapiens	HUMA- Human polypeptide SEQ ID NO 1985.	81	29
1660	gi2058326	Homo sapiens	subunit of RNA polymerase II transcription factor TFIID	5311	97
1660	AAU82954	Homo sapiens	ANAD- Human homologue of MPT1 protein target for antifungal compound.	4810	89
1660	gi1732073	Homo sapiens	TBP-associated factor	4736	99
1661	gi903599	Homo sapiens	Krueppel-type zinc finger protein	2690	97
1661	gi487783	Homo sapiens	zinc finger protein ZNF133	1503	49
1661	gi11137511	Homo sapiens	dJ568F9.1 (zinc finger protein 133 (clone pHZ-13))	1503	49
1662	gi13507379	Homo sapiens	BBS2	3715	100
1662	gi15559555	Homo sapiens	Bardet-Biedl syndrome 2	3710	99
1662	AAB93128	Homo sapiens	HELI- Human protein sequence SEQ ID NO:12015.	3684	99
1663	AAV73489	Homo sapiens	GEMY Human secreted protein clone yk84_1 protein sequence SEQ ID NO:200.	162	55

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SEQ ID	Hit ID	Species	Description	S score	Percent identity
1663	AAM93661	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3536.	79	53
1663	gi6690638	Bos taurus	N-type calcium channel alpha1B subunit	76	42
1664	AAV45305	Homo sapiens	HUMA- Human secreted protein fragment encoded from gene 6.	235	100
1664	gi 20903963 ref XP_139423.1	Mus musculus	similar to prune protein	66	48
1664	gi 18087604 gb AAL58932.1 AF462845.1	Arabidopsis thaliana	AT3g58560/F14P22_150	65	34
1665	gi7248794	Mus musculus	homeodomain protein	1115	73
1665	gi7248791	Mus musculus	homeobox protein	1115	73
1665	gi453172	Mus musculus	Sax-1	1115	73
1666	AAM79487	Homo sapiens	HYSE- Human protein SEQ ID NO 3133.	4868	99
1666	ABB11940	Homo sapiens	HYSE- Human secreted protein homologue, SEQ ID NO:2310.	4868	99
1666	AAM40565	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 5496.	4080	99
1667	AAM79487	Homo sapiens	HYSE- Human protein SEQ ID NO 3133.	4868	99
1667	ABB11940	Homo sapiens	HYSE- Human secreted protein homologue, SEQ ID NO:2310.	4868	99
1667	AAM40565	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 5496.	4080	99
1668	ABB44589	Homo sapiens	SWIT- Human wound healing related polypeptide SEQ ID NO 46.	727	83
1668	AAW13005	Homo sapiens	INCY- Human homologue of rat PRL-1 (HPRL).	727	83
1668	gi894159	Homo sapiens	protein-tyrosine phosphatase	727	83
1669	gi1752736	Saccharomyces cerevisiae	gene required for phosphorylation of oligosaccharides/ has high homology with YJR061w	180	40
1669	AAM39441	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2586.	173	29
1669	gi2292986	Rattus norvegicus	cyclic nucleotide-gated channel beta subunit	168	36
1670	gi17390151	Homo sapiens	Similar to RIKEN cDNA 2410088E07 gene	1538	96
1670	AAB93089	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11933.	508	47
1670	AAB95132	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17140.	174	43
1671	AAB94103	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14326.	3166	100
1671	gi11643582	Homo sapiens	PR-domain containing protein 14	3166	100
1671	gi8575782	Homo sapiens	PR-domain zinc finger protein 6 isoform A; PR-domain family protein 3 isoform A; PRDM6A; PFM3A	444	28
1672	AAM42499	Homo sapiens	HUMA- Human kidney related polypeptide SEQ ID NO 368.	516	98
1672	AAM99684	Homo sapiens	HUMA- Human excretory related	516	98

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SEQ ID	Hit ID	Species	Description	S score	Percent identity
			polypeptide SEQ ID NO 421.		
1673	ABB04729	Homo sapiens	SHAN- Human PP3501 protein SEQ ID NO:14.	775	100
1673	gi14329727	Secale cereale	high molecular weight glutenin subunit y	80	25
1673	gi6684164	Triticum aestivum	glutenin, high molecular weight subunit type y precursor	77	27
1674	gi6572186	Homo sapiens	dJ127B20.3 (novel PHD finger protein)	1506	100
1674	AAB94512	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15225.	753	38
1674	gi20135652	Homo sapiens	BRAF35/HDAC2 complex 80 kDa protein	753	38
1675	gi21435965	Mus musculus	L-threonine 3-dehydrogenase	547	57
1675	gi19526267	Takifugu rubripes	threonine dehydrogenase	321	48
1675	gi16183138	Drosophila melanogaster	GH18546p	294	42
1676	gi338088	Homo sapiens	SIL	73	31
1676	gi13991571	Homo sapiens	SIL protein	73	31
1676	gi18597271 ref XP_090831.1	Homo sapiens	similar to bB128O4.1.1 (novel protein)	337	86
1677	AAB94389	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14949.	2816	100
1677	AAB93905	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13864.	2810	99
1677	AAG73977	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:4741.	490	100
1678	gi15215485	Homo sapiens	Similar to RIKEN cDNA 2610002K22 gene	1495	99
1678	ABB89668	Homo sapiens	HUMA- Human polypeptide SEQ ID NO 2044.	710	77
1678	gi11762184	Arabidopsis thaliana	AT3g07750	500	38
1679	AAB95488	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18023.	793	100
1679	gi1408182	Homo sapiens	LGN protein	88	32
1679	gi18204662	Mus musculus	Similar to LGN protein	88	32
1680	gi18147099	Homo sapiens	zinc finger protein N27C7	2487	100
1680	gi488555	Homo sapiens	zinc finger protein ZNF135	1245	57
1680	gi15012179	Homo sapiens	zinc finger protein 16 (KOX 9)	1184	59
1681	gi21064943	Homo sapiens	FYVE-RING finger protein SAKURA	1064	97
1681	gi16904134	Homo sapiens	fring	1064	97
1681	gi20306347	Homo sapiens	Similar to fring	1048	98
1682	AAM25840	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1355.	270	89
1683	AAU84289	Homo sapiens	BGHM Human endometrial cancer related protein, KRT8.	865	59
1683	gi1673575	org=human] human cytokeratin 8 [Homo sapiens		865	59
1683	gi400416	Homo sapiens	Keratin 8	865	59
1684	gi11494213	Homo sapiens	Mix.1 homeobox-like protein	1221	100
1684	gi12698336	Homo sapiens	homeodomain protein MIX	1221	100

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SEQ ID	Hit ID	Species	Description	S score	Percent identity
1684	gi4585580	Mus musculus	Mix-like homeobox protein	779	69
1685	gi18034078	Homo sapiens	SPRY domain-containing SOCS box protein SSB-4	1442	100
1685	gi18034072	Homo sapiens	SPRY domain-containing SOCS box protein SSB-1	1117	74
1685	gi18034092	Mus musculus	SPRY domain-containing SOCS box protein SSB-1	1110	74
1686	AAB36607	Homo sapiens	INCY- Human FLEXHT-29 protein sequence SEQ ID NO:29.	1244	100
1686	AAU28346	Homo sapiens	HYSE- Novel human secretory protein, Seq ID No 703.	1244	100
1686	AAU28158	Homo sapiens	HYSE- Novel human secretory protein, Seq ID No 327.	1244	100
1687	AAB36607	Homo sapiens	INCY- Human FLEXHT-29 protein sequence SEQ ID NO:29.	1459	100
1687	AAU28346	Homo sapiens	HYSE- Novel human secretory protein, Seq ID No 703.	1459	100
1687	gi10803417	Homo sapiens	GPP34-related protein	1459	100
1688	gi14804	Bacteriophage phi-80	cI gene (AA 1 - 236)	1236	100
1688	gi476017	Pectobacterium carotovorum	pectin lyase regulation DNA-binding protein	694	58
1688	gi5725181	Pseudomonas aeruginosa	PRF4	427	40
1689	gi4704279	Schizosaccharomyces pombe	set domain protein; transcriptional silencing	561	45
1689	gi18376303	Neurospora crassa	related to regulatory protein SET1	543	46
1689	gi529135	Saccharomyces cerevisiae	Set1p	519	37
1690	AAU12290	Homo sapiens	GETH Human PRO6093 polypeptide sequence.	750	100
1690	AAG68333	Homo sapiens	LEXI- Human lipocalin homologue NHP protein SEQ ID NO:26.	743	98
1690	AAG68329	Homo sapiens	LEXI- Human lipocalin homologue NHP protein SEQ ID NO:18.	743	98
1691	AAG67394	Homo sapiens	SUGE- Amino acid sequence of human protein kinase SGK269.	4367	98
1691	gi18676662	Homo sapiens	FLJ00230 protein	1751	97
1691	gi557822	Saccharomyces cerevisiae	mal5, sta1, len: 1367, CAI: 0.3, AMYH_YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	207	21
1692	gi5679450	Homo sapiens	dJ153G14.3 (novel C2H2 type Zinc Finger protein)	1825	100
1692	AAG66311	Homo sapiens	BIOD- Human zinc finger protein 46.	1034	58
1692	gi19548796	Mus musculus	multifinger protein mKr2	1015	57
1693	AAM48334	Homo sapiens	UYNA- Human specific protein kinase NYD-SP15.	845	100
1693	gi13311007	Homo sapiens	protein kinase NYD-SP15	845	100
1693	gi12666210	Homo sapiens	bA103J18.2 (novel protein)	717	100
1694	AAM58279	Homo sapiens	MOLE- Human brain expressed single exon probe encoded protein SEQ ID NO: 30384.	506	100
1694	gi786117	Ensis minor	nuclear protein	238	34
1694	gi5821153	Homo sapiens	RNA binding protein	236	29

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1695	AAO08301	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 22193.	2088	100
1695	gi17026376	Mus musculus	muscle-derived protein MDP77 variant 2	1362	68
1695	gi17026374	Mus musculus	muscle-derived protein MDP77 variant 1	1362	68
1696	AAO08302	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 22194.	513	100
1696	gi337493	Homo sapiens	ribosomal protein L18	309	69
1696	gi206724	Rattus norvegicus	ribosomal protein L18	291	67
1697	gi21064613	Drosophila melanogaster	RE60835p	523	45
1697	AAG01784	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 5865.	471	100
1697	AAM41425	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 6356.	398	97
1698	gi13559033	Homo sapiens	bA11M20.3.1 (novel protein similar to Pleurodeles waltlii RAP55 protein, isoform 1)	1985	100
1698	gi13559032	Homo sapiens	bA11M20.3.2 (novel protein similar to Pleurodeles waltlii RAP55 protein, isoform 2)	1259	90
1698	AAB54170	Homo sapiens	HUMA- Human pancreatic cancer antigen protein sequence SEQ ID NO:622.	1225	98
1699	AAO12584	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 26476.	677	99
1699	gi2253297	Monodelphis domestica	kinesin homolog	565	80
1699	gi1572665	Dictyostelium discoideum	kinesin-like protein K6	452	46
1700	gi13016757	Homo sapiens	dJ553F4.3 (novel zinc-finger protein)	1278	99
1700	AAB95176	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17237.	1265	98
1700	AAO09518	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 23410.	932	100
1701	AAB61163	Homo sapiens	CHIR Human BBSR Gene X protein.	1178	92
1701	AAB94528	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15257.	1178	92
1701	AAM41708	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 6639.	1178	92
1702	gi2995589	Leishmania major	L2759.5	105	25
1702	AAR87539	Homo sapiens	UYWA- Polycystic kidney disease 1 polypeptide (polycystin).	98	24
1702	AAR87538	Homo sapiens	UYWA- Polycystic kidney disease 1 protein (polycystin) fragment.	98	24
1703	AAB30845	Homo sapiens	LEXI- Amino acid sequence of human signal transduction protein SGT5-17.	1288	99
1703	AAB30844	Homo sapiens	LEXI- Amino acid sequence of human signal transduction protein SGT5-15.	1288	99
1703	AAB30835	Homo sapiens	LEXI- Amino acid sequence of human signal transduction protein SGT5-8.	1288	99
1704	gi200964	Mus musculus	serine 2 ultra high sulfur protein	281	48

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SEQ ID	Hit ID	Species	Description	S score	Percent identity
1704	gi200962	Mus musculus	serine 1 ultra high sulfur protein	278	40
1704	AAM39466	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2611.	267	39
1705	gi4416181	Mus musculus	ES18	2258	88
1705	gi4416183	Homo sapiens	ES18	1106	98
1705	AAB38555	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 34 SEQ ID NO:92.	721	90
1706	gi188882	Homo sapiens	mucin	2151	75
1706	gi14973269	Streptococcus pneumoniae TIGR4	cell wall surface anchor family protein	1255	24
1706	gi17384256	Homo sapiens	mucin 5	1189	31
1707	AAW59357	Homo sapiens	UYNY- Human retinal degeneration B1 polypeptide (hrdgB1).	5070	99
1707	gi12667440	Homo sapiens	NIR1	5070	99
1707	gi5771350	Mus musculus	M-RdgB2 retinal degeneration protein B subtype 2	2779	56
1708	gi14328881	Cricetulus griseus	RNA polymerase II largest subunit	601	40
1708	gi200794	Mus musculus	RNA polymerase II	601	40
1708	gi387055	Cricetulus griseus	RNA polymerase II largest subunit	601	40
1709	AAU15995	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 948.	1617	90
1709	gi2618752	Takifugu rubripes	zinc finger protein	1307	67
1709	AAU16432	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 1385.	819	100
1710	AAU15995	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 948.	1816	100
1710	gi2618752	Takifugu rubripes	zinc finger protein	1495	75
1710	AAU16432	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 1385.	819	100
1711	AAB53356	Homo sapiens	HUMA- Human colon cancer antigen protein sequence SEQ ID NO:896.	2987	95
1711	gi15530243	Homo sapiens	Similar to villin 2 (ezrin)	2987	95
1711	AAV27443	Homo sapiens	CNRS Amino acid sequence of human ezrin polypeptide.	2984	95
1712	AAB53356	Homo sapiens	HUMA- Human colon cancer antigen protein sequence SEQ ID NO:896.	2764	90
1712	gi15530243	Homo sapiens	Similar to villin 2 (ezrin)	2764	90
1712	AAV27443	Homo sapiens	CNRS Amino acid sequence of human ezrin polypeptide.	2761	90
1713	AAB53356	Homo sapiens	HUMA- Human colon cancer antigen protein sequence SEQ ID NO:896.	2959	93
1713	gi15530243	Homo sapiens	Similar to villin 2 (ezrin)	2959	93
1713	AAV27443	Homo sapiens	CNRS Amino acid sequence of human ezrin polypeptide.	2956	93
1714	gi9963808	Homo sapiens	sentrin/SUMO-specific protease	1253	100
1714	gi16550940	Homo sapiens	SUMO-1 specific protease 2	1174	99
1714	ABB04392	Homo sapiens	BODE- Human protein phosphatase 24.53 SEQ ID NO 2.	1169	99
1715	AAG66311	Homo sapiens	BIOD- Human zinc finger protein 46.	1266	62

Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1715	gi488555	Homo sapiens	zinc finger protein ZNF135	1258	60
1715	gi5441615	Canis familiaris	zinc finger protein	1253	59
1716	AAE03642	Homo sapiens	INCY- Human extracellular matrix and cell adhesion molecule-6 (XMAD-6).	1878	100
1716	AAG93286	Homo sapiens	NISC- Human protein HP10648.	1878	100
1716	gi17945507	Drosophila melanogaster	RE23450p	258	44
1717	AAM93699	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3620.	2021	100
1717	gi15929609	Homo sapiens	Similar to RIKEN cDNA 2410081M15 gene	2021	100
1717	gi17160889	Mus musculus	RIKEN cDNA 2410081M15 gene	1671	81
1718	AAB07704	Homo sapiens	INMR Protein encoded by the endogenetic fragment of HERV-W.	323	42
1718	gi8272464	Homo sapiens	gag	323	42
1718	AAB07703	Homo sapiens	INMR Protein encoded by the endogenetic fragment of HERV-W.	307	39
1719	gi15990498	Homo sapiens	Similar to RIKEN cDNA 2310028H24 gene	1035	100
1719	gi7209311	Homo sapiens	FLJ00005 protein	510	100
1719	ABB17315	Homo sapiens	HUMA- Human nervous system related polypeptide SEQ ID NO 5972.	201	89
1720	AAB93829	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13646.	849	100
1720	AAB47278	Homo sapiens	MYRI- PN7771.	262	41
1720	gi13518076	Homo sapiens	ninein centrosomal protein isoform B	262	41
1721	gi18146756	Homo sapiens	limkain beta 2	1681	100
1721	AAAY86509	Homo sapiens	HUMA- Human gene 70-encoded protein fragment, SEQ ID NO:424.	696	100
1721	AAAY86510	Homo sapiens	HUMA- Human gene 70-encoded protein fragment, SEQ ID NO:425.	436	100
1722	gi14039857	Homo sapiens	testes development-related NYD-SP22	275	92
1722	gi19528401	Drosophila melanogaster	RE10196p	73	37
1722	gi21362074 ref NP_115 985.2	Homo sapiens	testes development-related NYD-SP22	711	100
1723	AAAY21623	Homo sapiens	REGC Ligand binding domain of nuclear receptor hGR.	2027	100
1723	AAP80919	Homo sapiens	SALK Sequence of the primary protein sequence of human glucocorticoidreceptor (hGR).	2027	100
1723	gi31682	Homo sapiens	beta-glucocorticoid receptor	2027	100
1724	gi16505737	Homo sapiens	NSE1 protein	1570	99
1724	gi20070972	Homo sapiens	similar to NSE1 protein	1569	99
1724	gi13529542	Mus musculus	RIKEN cDNA 4731402F03 gene	1525	96
1725	gi183780	Homo sapiens	apurinic/apyrimidinic endonuclease	1573	94
1725	gi254069	Homo sapiens	Ref-1	1573	94
1725	gi32022	Homo sapiens	AP endonuclease 1	1573	94
1726	AAG75675	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:6439.	142	39
1726	gi13661166	Mus musculus	bHLH factor Hes7	91	30
1726	gi5821140	Homo sapiens	ASY	90	31
1727	AAG03366	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 7447.	355	97

Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1727	gi4098861	Homo sapiens	transcription factor	89	32
1727	gi1419546	Gallus gallus	tenascin Y variant	83	39
1728	AAB70692	Homo sapiens	CHUS Human DEC2a protein sequence SEQ ID NO:2.	2509	100
1728	gi12583669	Homo sapiens	bHLH protein DEC2	2509	100
1728	gi19684064	Homo sapiens	basic helix-loop-helix domain containing, class B, 3	2505	99
1729	gi11345048	Homo sapiens	SCAN domain-containing protein 2	1607	99
1729	gi11320940	Homo sapiens	SCAND2	1607	99
1729	AAB95179	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17243.	708	100
1731	AAE10812	Homo sapiens	FARB Human agmatinase.	1833	99
1731	gi18031951	Homo sapiens	agmatinase	1833	99
1731	AAE10813	Homo sapiens	FARB Human vector-trimmed agmatinase.	1830	99
1732	gi31799	Homo sapiens	glutamate dehydrogenase	1453	98
1732	gi31707	Homo sapiens	GDH	1453	98
1732	gi183060	Homo sapiens	glutamate dehydrogenase precursor (EC 1.4.1.3.)	1453	98
1733	gi13905148	Mus musculus	RIKEN cDNA 5430417M23 gene	1396	83
1733	AAM95516	Homo sapiens	HUMA- Human reproductive system related antigen SEQ ID NO: 4174.	740	91
1733	gi439146	Saccharomyces cerevisiae	B-type cyclin	90	32
1734	gi13936547	Homo sapiens	formin-binding protein 17	3194	100
1734	gi20196204	Rattus norvegicus	rapostlin	2985	93
1734	AAB94690	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15657.	2983	95
1735	AAV83093	Homo sapiens	UYNV F-box protein FBP-25.	1002	100
1735	gi6164743	Homo sapiens	F-box protein Fbx20	1002	100
1735	AAV83072	Homo sapiens	UYNV F-box motif of FBP-25.	261	100
1736	gi21450559	Caenorhabditis elegans	C. elegans PQN-34 protein (corresponding sequence F35B3.5)	131	28
1736	gi21323260	Corynebacterium glutamicum ATCC 13032	Translation elongation and release factors (GTPases)	78	27
1736	gi9826	Plasmodium falciparum	11-1 polypeptide	74	24
1737	gi14530677	Homo sapiens	WNT14	1610	98
1737	gi18656356	Mus musculus	Wnt14	1593	97
1737	gi2623871	Gallus gallus	Wnt-14 protein	1400	85
1738	gi14530677	Homo sapiens	WNT14	1804	97
1738	gi18656356	Mus musculus	Wnt14	1779	95
1738	gi2623871	Gallus gallus	Wnt-14 protein	1543	82
1739	ABB05686	Homo sapiens	GEHU- Human amygdala derived protein clone amy2_2a13.	2046	88
1739	AAG93283	Homo sapiens	NISC- Human protein HP10626.	321	64
1739	gi15559443	Homo sapiens	Similar to RIKEN cDNA 2810417J12 gene	321	64
1740	AAB94660	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15579.	886	98
1740	gi2769562	Homo sapiens	ZYG homologue	655	27
1740	AAM40229	Homo sapiens	HYSE- Human polypeptide SEQ ID	653	30

Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
			NO 3374.		
1741	gi2984386	Aquifex aeolicus	processing protease	73	24
1741	gi 21298588 gb EAA10733.1	Anopheles gambiae str. PEST	ebiP4413	605	59
1741	gi 18396588 ref NP_566209.1	Arabidopsis thaliana	expressed protein	385	43
1742	AAM41554	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 6485.	999	53
1742	AAG00335	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 4416.	863	99
1742	gi18606006	Mus musculus	Similar to RIKEN cDNA 9430059D04 gene	798	56
1743	AAB08622	Homo sapiens	MILL- Amino acid sequence of a human DRT111 polypeptide.	1470	99
1743	gi14043850	Homo sapiens	Similar to splicing factor (45kD)	1470	99
1743	gi3746840	Homo sapiens	45kDa splicing factor; SPF 45	1460	98
1744	gi17105197	Homo sapiens	kelch-like protein KLHL6	3200	99
1744	gi14020951	Homo sapiens	FLJ00029 protein	1293	99
1744	gi18204103	Mus musculus	RIKEN cDNA 4930429H24 gene	1131	46
1745	AAM85059	Homo sapiens	HUMA- Human immune/haematopoietic antigen SEQ ID NO:12652.	398	100
1745	AAG02849	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 6930.	301	98
1745	AAM74469	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 34775.	207	100
1746	AAE18209	Homo sapiens	CURA- Human MOL2 protein.	1013	46
1746	AAG67510	Homo sapiens	SMIK Amino acid sequence of a human secreted polypeptide.	1013	46
1746	AAM66605	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 26911.	1013	46
1747	gi10944334	Homo sapiens	Hu-Claspin	6812	99
1747	gi10944336	Xenopus laevis	Claspin	2576	46
1747	gi13559049	Homo sapiens	bA435D7.1.2 (novel protein)	2355	100
1748	AAM00966	Homo sapiens	HYSE- Human bone marrow protein, SEQ ID NO: 442.	144	52
1748	gi 17545798 ref NP_519200.1	Ralstonia solanacearum	PROBABLE GLUCARATE DEHYDRATASE PROTEIN	68	24
1749	gi12328443	Homo sapiens	PAPA-1	1810	99
1749	gi12328441	Mus musculus	PAPA-1	1693	93
1749	gi18044415	Mus musculus	RIKEN cDNA 2510009I23 gene	1693	93
1750	gi20515250	Thermoanaerobacter tengcongensis	Threonine aldolase	247	37
1750	gi11762214	Arabidopsis thaliana	AT3g04520	239	42
1750	gi4982322	Thermotoga maritima	L-allo-threonine aldolase	234	40
1751	gi1854550	Mus musculus	red-1	607	96
1751	gi13435627	Mus musculus	Similar to nucleoredoxin	607	96

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Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1751	gi4056568	Zea mays	PDI-like protein	121	30
1752	gi10440418	Homo sapiens	FLJ00044 protein	2020	66
1752	AAB93931	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13927.	1083	66
1752	AAM85707	Homo sapiens	HUMA- Human immune/haematopoietic antigen SEQ ID NO:13300.	441	73
1753	AAM39300	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2445.	224	30
1753	AAM79228	Homo sapiens	HYSE- Human protein SEQ ID NO 1890.	224	30
1753	AAM41086	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 6017.	223	30
1754	AAV07867	Homo sapiens	HUMA- Human secreted protein fragment encoded from gene 16.	872	90
1754	AAW71684	Homo sapiens	INCY- Amino acid sequence of the human tumourigenesis associated protein.	872	90
1754	gi5531811	Homo sapiens	BUP	872	90
1755	AAS16923_aal	Homo sapiens	UYNA- Human testis protein kinase cDNA.	1884	99
1755	AAU11260	Homo sapiens	UYNA- Human testis protein kinase.	1884	99
1755	gi10799166	Homo sapiens	protein kinase Njmu-R1	1884	99
1756	AAM75106	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 35412.	241	100
1756	AAM62303	Homo sapiens	MOLE- Human brain expressed single exon probe encoded protein SEQ ID NO: 34408.	241	100
1756	gi7021367	Drosophila melanogaster	c11.1	121	19
1757	AAM75106	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 35412.	241	100
1757	AAM62303	Homo sapiens	MOLE- Human brain expressed single exon probe encoded protein SEQ ID NO: 34408.	241	100
1757	gi7021367	Drosophila melanogaster	c11.1	108	19
1758	gi14547148	Homo sapiens	EGLN2 protein	2183	100
1758	gi18031805	Homo sapiens	estrogen-induced tag 6	2176	99
1758	gi18182546	Mus musculus	EGLN2	1926	87
1759	gi16566668	Homo sapiens	dachshund 2	817	99
1759	AAM75993	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 36299.	812	99
1759	AAM69137	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 29443.	812	99
1760	AAB74314	Homo sapiens	UYFU- Human splicing factor 2 protein.	722	100
1760	AAM41646	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 6577.	722	100
1760	AAB92868	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11452.	616	99

Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1761	gi12314095	Homo sapiens	dJ412I7.1 (similar to radial spokehead protein)	2575	99
1761	gi13345407	Mus musculus	radial spokehead-L protein	1824	52
1761	gi2905895	Strongylocentrotus purpuratus	radial spokehead	1692	61
1762	AAM79056	Homo sapiens	HYSE- Human protein SEQ ID NO 1718.	972	52
1762	gi2529737	Xenopus laevis	ER1	968	44
1762	AAAY15835	Homo sapiens	PATE/ A human er1 protein.	963	52
1763	AAB95581	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18241.	2949	99
1763	AAU17430	Homo sapiens	HUMA- Novel signal transduction pathway protein, Seq ID 995.	298	46
1763	gi3184264	Homo sapiens	F02569_2	169	45
1764	AAAY59288	Homo sapiens	ORDE- Human MUC11 polypeptide.	4817	99
1764	gi5911171	Homo sapiens	mucin 11	4817	99
1764	gi14973269	Streptococcus pneumoniae TIGR4	cell wall surface anchor family protein	841	24
1765	gi12038915	Homo sapiens	dJ1002M8.3 (novel protein)	1204	100
1765	gi11602976	Homo sapiens	dJ1178H5.4.1 (Novel protein (isoform 1))	938	100
1765	gi13559286	Homo sapiens	dJ1178H5.4.3 (novel protein (isoform 3))	901	99
1766	AAM79884	Homo sapiens	HYSE- Human protein SEQ ID NO 3530.	8899	92
1766	AAM79883	Homo sapiens	HYSE- Human protein SEQ ID NO 3529.	8899	92
1766	AAM78899	Homo sapiens	HYSE- Human protein SEQ ID NO 1561.	8408	92
1767	AAB94757	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15817.	489	51
1767	AAM40651	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 5582.	489	51
1767	AAM38865	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2010.	489	51
1768	gi18447198	Drosophila melanogaster	GH09355p	115	27
1768	gi21428632	Drosophila melanogaster	LP07116p	112	25
1768	gi14915682	Streptococcus pyogenes	fibronectin-binding protein Fba	111	27
1769	gi15147877	Mus musculus	Spred-2	1170	92
1769	AAU17415	Homo sapiens	HUMA- Novel signal transduction pathway protein, Seq ID 980.	1029	98
1769	gi15147875	Mus musculus	Spred-1	504	46
1770	gi18252391	Xenopus laevis	noelin-1	358	32
1770	gi18252389	Xenopus laevis	noelin-2	358	32
1770	AAU81220	Homo sapiens	CORI- Human lung cancer protein, Seq ID No 39.	355	33
1771	gi9930614	Homo sapiens	steroid receptor RNA activator isoform 3	1241	100
1771	gi9930610	Homo sapiens	steroid receptor RNA activator isoform 1	1221	99
1771	gi9930612	Homo sapiens	steroid receptor RNA activator isoform	1215	98

Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
			2		
1772	gi18204103	Mus musculus	RIKEN cDNA 4930429H24 gene	541	30
1772	gi2282582	Mus musculus	actin-binding protein	457	28
1772	gi17105197	Homo sapiens	kelch-like protein KLHL6	457	26
1773	AAU16201	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 1154.	279	100
1773	AAU16614	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 1567.	273	98
1773	gi2605924	Dictyostelium discoideum	histidine kinase C	71	36
1774	gi1881236	Bacillus subtilis	PROBABLE DNA TOPOISOMERASE III	85	25
1774	gi2632726	Bacillus subtilis	DNA topoisomerase III	85	25
1774	gi7882853	Leishmania major	511.3	85	25
1775	gi17135102	Nostoc sp. PCC 7120	leucine-rich-repeat protein	251	30
1775	gi16307072	Homo sapiens	Similar to RIKEN cDNA 2010005E21 gene	251	33
1775	AAB26846	Homo sapiens	NAKA/ Human MASL1 protein sequence.	245	33
1776	gi3549261	Dictyostelium discoideum	interaptin	162	25
1776	gi3694990	Mus musculus	alpha-actinin 3	146	22
1776	gi8096219	Drosophila melanogaster	Trio	145	20
1777	gi1780976	Human endogenous retrovirus K	protease	889	58
1777	gi9558703	Homo sapiens	protease	883	59
1777	gi5802824	Homo sapiens	Gag-Pro-Pol protein	839	59
1778	gi15990408	Homo sapiens	homeo box B9	1334	100
1778	gi11993915	Homo sapiens	HOXB9	1334	100
1778	gi440955	Mus sp.	Drosophila Abdominal-B homolog	1285	96
1779	AAU08663	Homo sapiens	CURA- Human NOV7 protein.	1654	99
1779	gi20809594	Homo sapiens	CTCL tumor antigen se57-1	1654	99
1779	AAU08662	Homo sapiens	CURA- Human NOV6 protein.	1649	99
1780	AAO14212	Homo sapiens	INCY- Human transporter and ion channel TRICH-29.	917	100
1780	AAE04897	Homo sapiens	INCY- Human transporter and ion channel-10 (TRICH-10) protein.	693	76
1780	AAM40059	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 3204.	693	76
1781	gi3139158	Homo sapiens	LINE-1 like protein	318	100
1781	AAB64943	Homo sapiens	ROSE/ Human secreted protein sequence encoded by gene 7 SEQ ID NO:121.	154	46
1781	gi558908	Mus musculus	reverse transcriptase	154	47
1782	gi6841266	Homo sapiens	HSPC308	206	58
1782	AAM39632	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2777.	205	50
1782	AAO04405	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 18297.	202	58
1783	AAG01500	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 5581.	515	99

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Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1783	gi9799628	Drosophila melanogaster	Nut2	405	60
1783	gi21392250	Drosophila melanogaster	SD24044p	405	60
1784	AAM71079	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 31385.	84	42
1784	AAM58578	Homo sapiens	MOLE- Human brain expressed single exon probe encoded protein SEQ ID NO: 30683.	84	42
1784	gi406049	Manduca sexta	chitinase precursor	79	36
1785	gi10580910	Halobacterium sp. NRC-1	Vng1407c	83	48
1785	gi2635307	Bacillus subtilis	ysmA	71	27
1785	gi 20911067 ref XP_130444.1	Mus musculus	RIKEN cDNA 0610012H03	273	64
1786	gi13539682	Homo sapiens	golgi-associated microtubule-binding protein HOOK3	2320	100
1786	gi5706448	Homo sapiens	dJ782L23.1 (HOOK1)	1421	61
1786	gi3005085	Homo sapiens	hook1 protein	1421	61
1787	AAM93845	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3925.	1379	99
1787	AAO06616	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 20508.	852	98
1787	gi8118231	Homo sapiens	B17	836	100
1788	ABB50189	Homo sapiens	INCY- Human transcription factor TRFX-40.	1470	100
1788	gi17945101	Drosophila melanogaster	RE08174p	230	34
1788	gi9965418	Mus musculus	iroquois-class homeobox protein IRX2	206	45
1789	AAM68691	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 28997.	743	94
1789	AAM68095	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 28401.	743	94
1789	AAM56316	Homo sapiens	MOLE- Human brain expressed single exon probe encoded protein SEQ ID NO: 28421.	743	94
1790	gi17390973	Mus musculus	RIKEN cDNA 4930449E07 gene	859	85
1790	gi16755788	Drosophila melanogaster	protein phosphatase regulatory subunit short isoform	340	41
1790	gi16519039	Drosophila melanogaster	protein phosphatase 1 regulatory subunit	340	41
1791	AAM93401	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3002.	3580	98
1791	AAU15960	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 913.	558	92
1791	AAU16404	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 1357.	524	91
1792	gi1163177	Homo sapiens	inducible poly(A)-binding protein	1444	75
1792	gi2801403	Homo sapiens	polyadenylate binding protein	1444	75
1792	gi19526272	Takifugu rubripes	polyA-binding protein	1443	75

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Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1793	gi13276231	Homo sapiens	FYVE and coiled-coil domain containing 1	1881	99
1793	gi18250726	Mus musculus	FYVE and coiled-coil domain containing 1	1670	87
1793	gi18676678	Homo sapiens	FLJ00238 protein	982	100
1794	gi15384740	Homo sapiens	paralemmin-2	1237	99
1794	gi15384742	Homo sapiens	Palm2-AKAP2 fusion protein	1166	100
1794	gi4456148	Gallus gallus	paralemmin	364	37
1795	AAM69584	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 29890.	1382	98
1795	AAM57181	Homo sapiens	MOLE- Human brain expressed single exon probe encoded protein SEQ ID NO: 29286.	1382	98
1795	gi600118	Zea mays	extensin-like protein	234	26
1796	gi19911907	Hepatitis C virus type 1b	polyprotein	72	36
1796	gi14150633	Hepatitis C virus	NS3 protease	72	36
1796	ABB89981	Homo sapiens	HUMA- Human polypeptide SEQ ID NO 2357.	70	32
1797	AAB94534	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15270.	1978	100
1797	AAM94023	Homo sapiens	HELI- Human stomach cancer expressed polypeptide SEQ ID NO 116.	1978	100
1797	AAM92201	Homo sapiens	HUMA- Human digestive system antigen SEQ ID NO: 1550.	1760	100
1798	gi18447158	Drosophila melanogaster	AT31457p	461	36
1798	AAM40345	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 3490.	430	45
1798	gi6166507	Mus musculus	RP42	418	43
1799	gi13278936	Homo sapiens	Similar to RIKEN cDNA 5430432M24 gene	1527	100
1799	gi12734105	Homo sapiens	bA371L19.3 (novel protein)	1527	100
1799	gi18044114	Mus musculus	RIKEN cDNA 9030611O19 gene	256	37
1800	AAE13811	Homo sapiens	CORI- Human lung tumour-specific protein SAL-104.	2405	100
1800	AAB43833	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:1278.	860	100
1800	AAB95292	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17515.	307	23
1801	AAB95536	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18138.	2116	99
1801	gi6409345	Homo sapiens	zinc finger protein ZNF180	953	41
1801	gi8050899	Homo sapiens	ZNF180	952	41
1802	ABB50181	Homo sapiens	INCY- Human transcription factor TRFX-32.	1050	100
1802	AAB58802	Homo sapiens	HUMA- Breast and ovarian cancer associated antigen protein sequence SEQ ID 510.	1050	100
1802	gi532313	Homo sapiens	NF45 protein	1050	100
1803	gi10644754	Caenorhabditis elegans	GATA-type transcription factor	83	33
1803	gi3880139	Caenorhabditis	Similarity to Yeast nitrogen regulatory	83	33

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Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
		elegans	protein GLN3 (PIR Acc. No. S22280), contains similarity to Pfam domain: PF00320 (GATA zinc finger), Score=20.9, E-value=0.0044, N=1		
1803	gi336134	Woodchuck hepatitis B virus	polymerase	78	40
1804	gi16076870	Drosophila melanogaster	LD37206p	521	48
1804	gi20334740	Arabidopsis thaliana	AT4g20350/F9F13_6	179	36
1804	AAG93258	Homo sapiens	NISC- Human protein HP10582.	147	26
1805	gi16076870	Drosophila melanogaster	LD37206p	341	54
1805	gi15155438	Agrobacterium tumefaciens str. C58 (Cereon)	AGR_C_894p	84	26
1805	gi9844612	Microcebus murinus	MHC class I antigen	77	30
1806	gi16076870	Drosophila melanogaster	LD37206p	333	51
1806	gi1592321	Methanococcus jannaschii	GMP synthase (guaA)	78	33
1806	gi15155438	Agrobacterium tumefaciens str. C58 (Cereon)	AGR_C_894p	77	26
1807	AAT86170_aa1	Homo sapiens	UYPA- Human Lasp-1 nucleotide sequence.	1190	86
1807	AAU09686	Homo sapiens	ICOS- Human LASP-1.	1190	86
1807	AAO13508	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 27400.	1190	86
1808	gi15823642	Homo sapiens	ALS2CR7	2038	100
1808	AAB65641	Homo sapiens	SUGE- Novel protein kinase, SEQ ID NO: 168.	1258	90
1808	gi2645810	Mus musculus	Pftaire-1	1195	68
1809	AAB95343	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17625.	2604	99
1809	AAB95767	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18699.	2273	100
1809	gi15808121	Homo sapiens	bA476B13.1 (novel protein)	918	100
1810	AAG01851	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 5932.	445	98
1810	gi483843	Bos taurus	50 kDa protein	86	35
1810	gi14028009	Mesorhizobium loti	probable malate dehydrogenase	71	27
1811	AAM79617	Homo sapiens	HYSE- Human protein SEQ ID NO 3263.	1635	99
1811	AAM78633	Homo sapiens	HYSE- Human protein SEQ ID NO 1295.	1598	100
1811	gi3402830	Homo sapiens	cE146D10.2 (mercaptopyruvate sulfurtransferase.(EC 2.8.1.2))	1598	100
1812	AAV00294	Homo sapiens	HUMA- Human secreted protein encoded by gene 37.	240	100
1812	gi5881743	Arabidopsis thaliana	NADH dehydrogenase ND5	76	33
1812	gi3366918	Arabidopsis	NADH dehydrogenase subunit F	76	33

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Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
		thaliana			
1813	gi18848219	Homo sapiens	similar to germinal center expressed transcript	715	100
1813	gi20987806	Homo sapiens	LOC205472	154	30
1813	gi1262852	Mus musculus	M17 protein	122	29
1814	AAM78520	Homo sapiens	HYSE- Human protein SEQ ID NO 1182.	526	65
1814	AAM79504	Homo sapiens	HYSE- Human protein SEQ ID NO 3150.	322	67
1814	gi20151641	Drosophila melanogaster	LD40094p	259	38
1815	AAB94396	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14964.	582	100
1815	AAB93300	Homo sapiens	HELI- Human protein sequence SEQ ID NO:12367.	477	54
1815	AAG64741	Homo sapiens	BIOD- Human zinc finger protein 57.	442	46
1816	gi915208	Sus scrofa	gastric mucin	299	28
1816	gi557822	Saccharomyces cerevisiae	mal5, sta1, len: 1367, CAI: 0.3, AMYH_YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	291	26
1816	gi1304387	Saccharomyces cerevisiae var. diastaticus	glucoamylase	291	26
1817	AAG73997	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:4761.	774	96
1817	gi2432007	Mus musculus	peripheral benzodiazepine receptor associated protein; PBR associated protein; PAP20	178	67
1817	gi7248371	Gallus gallus	myosin heavy chain	89	26
1818	AAB95103	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17076.	3402	99
1818	AAB94669	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15609.	2739	99
1818	gi6467206	Homo sapiens	gonadotropin inducible transcription repressor-4	1067	36
1819	AAG01908	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 5989.	307	100
1819	gi1246048	Saccharomyces cerevisiae	Mtr3p	69	27
1819	gi2313565	Helicobacter pylori 26695	virB4 homolog (virB4)	66	31
1820	AAM25844	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1359.	639	100
1820	AAM93795	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3825.	639	100
1820	AAG01158	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 5239.	502	100
1821	AAB67454	Homo sapiens	INCY- Amino acid sequence of a human chaperone polypeptide.	1097	99
1821	gi18028277	Homo sapiens	DnaJ protein SB73	1097	99
1821	gi20073291	Mus musculus	Similar to DnaJ protein SB73	985	88
1822	AAB93396	Homo sapiens	HELI- Human protein sequence SEQ ID NO:12579.	655	60
1822	gi3860093	Homo sapiens	MDC-3.13 isoform 2	655	60
1822	gi13937826	Homo sapiens	TNF-induced protein	655	60

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Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1823	AAG73872	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:4636.	584	78
1823	AAB03175	Homo sapiens	MITO- Human rad6 homologue UBC2.	584	78
1823	AAB43423	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:868.	584	78
1824	gi16306806	Homo sapiens	zinc finger protein 43 (HTF6)	951	28
1824	gi38032	Homo sapiens	ZNF43	950	28
1824	gi19851928	Homo sapiens	CLL-associated antigen KW-4 splice variant 2	929	29
1825	gi2749771	Mus musculus	tsec-1	1116	72
1825	gi4704204	Homo sapiens	dJ102D24.1 (novel Mitosis-specific Chromosome Segregation protein SMC1 LIKE protein)	146	24
1825	gi165490	Oryctolagus cuniculus	myosin heavy chain	143	20
1826	ABB16919	Homo sapiens	HUMA- Human nervous system related polypeptide SEQ ID NO 5576.	392	100
1826	gi19920045	Dictyostelium discoideum	UDP-glucose 4-epimerase	97	27
1826	AAM68085	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 28391.	90	22
1827	AAB36623	Homo sapiens	INCY- Human FLEXHT-45 protein sequence SEQ ID NO:45.	916	100
1827	gi20380177	Homo sapiens	Similar to RIKEN cDNA C330008K14 gene	916	100
1827	AAZ35834_aal	Homo sapiens	INCY- Human vesicle trafficking protein 2 encoding cDNA.	177	25
1828	gi20198331	Homo sapiens	apical protein 2	1316	98
1828	gi13543189	Mus musculus	Similar to RIKEN cDNA 1300007L22 gene	755	62
1828	AAM79494	Homo sapiens	HYSE- Human protein SEQ ID NO 3140.	305	38
1829	AAG01378	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 5459.	575	100
1829	AAW76636	Homo sapiens	FRAN/ Human cardiac HcTnT protein.	100	21
1829	gi408217	Homo sapiens	troponin T; TnT	100	21
1830	gi488555	Homo sapiens	zinc finger protein ZNF135	879	54
1830	AAB95862	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18929.	877	52
1830	gi13752754	Homo sapiens	zinc finger 1111	876	52
1831	AAE06678	Homo sapiens	INCY- Human nuclear hormone receptor (NHREC)-1 protein.	3211	100
1831	gi17026326	Homo sapiens	FKSG27	3211	100
1831	gi17026328	Mus musculus	FKSG27	2405	78
1832	AAB01386	Homo sapiens	INCY- Neuron-associated protein.	1558	98
1832	gi19421557	Homo sapiens	chromodomain helicase DNA binding protein 5	1554	97
1832	gi7799072	Homo sapiens	dJ540H1.1 (novel Helicase C-terminal domain and SNF2 N-terminal domains containing protein)	1352	100
1833	gi432544	Trichoplusia ni	HSUP59	74	41
1834	gi2394174	Homo sapiens	zinc finger protein ZNF191	801	56
1834	gi1698720	Homo sapiens	zinc finger protein	801	56
1834	gi4405797	Homo sapiens	retinoic acid suppression protein A	801	56

Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1835	gi20071535	Mus musculus	RIKEN cDNA 3222401M22 gene	366	31
1835	AAG73665	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:4429.	223	100
1835	gi3425860	Streptomyces coelicolor	ScbA protein	101	28
1836	gi20071535	Mus musculus	RIKEN cDNA 3222401M22 gene	339	28
1836	AAG73665	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:4429.	223	100
1836	gi392890	Homo sapiens	drebrin E2	94	28
1837	AAM71172	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 31478.	274	100
1837	AAM58666	Homo sapiens	MOLE- Human brain expressed single exon probe encoded protein SEQ ID NO: 30771.	274	100
1837	gi 21296312 gb EAA08457.1	Anopheles gambiae str. PEST	ebiP3199	524	30
1838	gi19070559	Xiphophorus maculatus	DM-domain containing transcription factor DMRT4	843	47
1838	gi9743439	Oreochromis niloticus	sex-determining protein DMO	795	45
1838	gi15216289	Oryzias latipes	OlaDMRT4	786	44
1839	AAB93901	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13855.	2946	99
1839	ABB04181	Homo sapiens	UROG- Human 34P3D7 protein.	2684	92
1839	gi13647045	Mus musculus	Slp homologue lacking C2 domains-a	1724	60
1840	AAB93901	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13855.	2907	95
1840	ABB04181	Homo sapiens	UROG- Human 34P3D7 protein.	2645	88
1840	gi13647045	Mus musculus	Slp homologue lacking C2 domains-a	1845	63
1841	ABB04181	Homo sapiens	UROG- Human 34P3D7 protein.	2735	99
1841	AAB93901	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13855.	2684	92
1841	gi13647045	Mus musculus	Slp homologue lacking C2 domains-a	1580	57
1842	AAB93901	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13855.	2675	92
1842	ABB04181	Homo sapiens	UROG- Human 34P3D7 protein.	2413	85
1842	gi13647045	Mus musculus	Slp homologue lacking C2 domains-a	1586	58
1843	AAB94395	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14962.	556	100
1843	gi17862960	Drosophila melanogaster	SD05477p	86	40
1843	gi2621988	Methanothermobacter thermotrophicus str. Delta H	integrase-recombinase protein	77	31
1844	AAU10981	Homo sapiens	BODE- Human aldehyde/ketone reductase 36.	1580	99
1844	AAM66435	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 26741.	588	100
1844	AAM54044	Homo sapiens	MOLE- Human brain expressed single exon probe encoded protein SEQ ID NO: 26149.	588	100

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Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1845	gi11994722	Arabidopsis thaliana	contains similarity to calmodulin~gene_id:F5N5.10	145	24
1845	gi21436047	Arabidopsis thaliana	AT3g22930/F5N5_10	145	24
1845	gi14625425	Nicotiana tabacum	calmodulin NtCaM13	138	27
1846	AAM89573	Homo sapiens	HUMA- Human immune/haematopoietic antigen SEQ ID NO:17166.	588	98
1846	AAB93031	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11803.	394	40
1846	gi2547025	Rattus norvegicus	XY40 protein	379	44
1847	AAB94676	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15624.	2317	99
1847	gi16769618	Drosophila melanogaster	LD44732p	89	29
1847	gi348245	Homo sapiens	protein serine/threonine kinase	84	22
1848	AAV59712	Homo sapiens	GEST Secreted protein 33-54-1-B9-FL1.	398	100
1848	gi8979275	Chlamydophila pneumoniae J138	muramoylalanine-glutamate ligase	81	26
1848	gi4377221	Chlamydophila pneumoniae CWL029	Muramoylalanine-Glutamate Ligase	81	26
1849	AAG80758	Homo sapiens	UYNA- Human testicular cytodifferentiation-related protein.	631	100
1849	gi9800509	Homo sapiens	pinch-2 protein	631	100
1849	AAG02299	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 6380.	428	98
1850	ABB06383	Homo sapiens	BODE- Human eukaryotic initiator 60 protein SEQ ID NO:2.	2720	94
1850	AAV73377	Homo sapiens	INCY- HTRM clone 1645941 protein sequence.	2720	94
1850	AAB94491	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15180.	2712	93
1851	AAM25737	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1252.	2203	100
1851	gi7920398	Homo sapiens	PTOV1	2152	98
1851	gi19353303	Mus musculus	expressed sequence AU041779	2151	96
1852	gi14588848	Homo sapiens	titin zinc-finger anchoring protein	1948	96
1852	gi13160386	Homo sapiens	ring finger protein 29	1870	96
1852	AAU15868	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 821.	1749	95
1853	AAB93042	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11827.	664	79
1853	AAB36613	Homo sapiens	INCY- Human FLEXHT-35 protein sequence SEQ ID NO:35.	254	74
1853	gi14603247	Homo sapiens	Similar to RIKEN cDNA 5730409G15 gene	254	74
1854	gi3387911	Homo sapiens	2-oxoglutarate carrier protein	1564	91
1854	gi23844	Homo sapiens	2-oxoglutarate carrier	1561	91
1854	gi18043006	Mus musculus	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	1515	88

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Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1855	AAE16790	Homo sapiens	INCY- Human transporter and ion channel-27 (TRICH-27) protein.	98	27
1855	AAM40851	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 5782.	97	31
1855	AAM39065	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2210.	97	31
1856	AAB56293	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 99 SEQ ID NO:387.	718	64
1856	AAM93941	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 4124.	552	41
1856	AAM93961	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 4169.	545	41
1857	gi12232322	Homo sapiens	hUPF3A	2480	100
1857	gi12620406	Homo sapiens	UPF3	2357	100
1857	AAM25610	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1125.	1922	91
1858	gi15823659	Homo sapiens	ALS2CR15	1816	98
1858	gi437664	Rattus norvegicus	autoantigen p69	668	43
1858	AAS03083_aal	Homo sapiens	HRCR- Human pancreatic beta-cell protein p69 cDNA sequence.	659	42
1859	AAB94387	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14945.	2182	100
1859	ABB10280	Homo sapiens	HUMA- Human cDNA SEQ ID NO: 588.	842	100
1859	ABB10478	Homo sapiens	HUMA- Human cDNA SEQ ID NO: 786.	556	94
1860	AAB95605	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18299.	2624	99
1860	gi212452	Gallus gallus	nonmuscle myosin heavy chain	1608	60
1860	gi7381235	Rattus norvegicus	nonmuscle myosin heavy chain-B	1598	59
1861	gi17390973	Mus musculus	RIKEN cDNA 4930449E07 gene	1400	80
1861	gi16519039	Drosophila melanogaster	protein phosphatase 1 regulatory subunit	438	35
1861	gi16755788	Drosophila melanogaster	protein phosphatase regulatory subunit short isoform	342	40
1862	gi9930784	Homo sapiens	dJ1158H2.1 (novel protein similar to D. melanogaster CG11048 and CG8959)	2051	100
1862	gi16768214	Drosophila melanogaster	GH24459p	1010	32
1862	AAB92852	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11417.	874	32
1863	AAB70366	Homo sapiens	HUMA- Human serine protease protein sequence SEQ ID NO:3.	1365	99
1863	AAH43519_aal	Homo sapiens	INCY- cDNA encoding protease PRTS-8.	1360	98
1863	AAB47566	Homo sapiens	INCY- Protease PRTS-8.	1360	98
1864	AAG02826	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 6907.	248	90
1865	gi20381091	Homo sapiens	similar to rab11-binding protein	1408	99
1865	gi4512103	Bos taurus	rab11 binding protein	1174	84
1865	gi6049150	Rattus	WD-containing protein	1023	78

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Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
		norvegicus			
1866	gi18447568	Drosophila melanogaster	RH09039p	357	32
1866	AAO03876	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 17768.	74	41
1866	gi 21290693 gb EAA02838.1	Anopheles gambiae str. PEST	agCP2341	256	37
1867	AAG93266	Homo sapiens	NISC- Human protein HP10200.	927	100
1867	AAV59763	Homo sapiens	META- Human normal ovarian tissue derived protein 40.	877	100
1867	gi20987329	Mus musculus	RIKEN cDNA 1110002H14 gene	812	91
1868	AAE19165	Homo sapiens	INCY- Human protease, PRTS-2 protein.	650	88
1868	AAG03616	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 7697.	429	96
1868	gi5002310	Caenorhabditis elegans	myotactin form A	78	23
1869	gi21392228	Drosophila melanogaster	RH61354p	517	29
1869	gi2114473	Mus musculus	p140mDia	503	28
1869	AAW76734	Homo sapiens	KIRI Human mDia Rho targeting protein.	501	27
1870	ABB16354	Homo sapiens	HUMA- Human nervous system related polypeptide SEQ ID NO 5011.	785	83
1870	gi21428564	Drosophila melanogaster	LD43055p	196	28
1870	gi16604458	Arabidopsis thaliana	At1g20130/T20H2_9	110	29
1871	AAM50328	Homo sapiens	MILL- Human nucleotide binding site protein NBS-5.	3117	100
1871	gi19387134	Homo sapiens	PYRIN-containing APAF1-like protein 4	3117	100
1871	gi19031214	Homo sapiens	PAAD and NACHT-containing protein 2	3117	100
1872	AAD24402 aa1	Homo sapiens	INCY- Human RNA metabolism protein-29 (RMEP-29) cDNA.	546	61
1872	AAE15266	Homo sapiens	INCY- Human RNA metabolism protein-29 (RMEP-29).	546	61
1872	AAB93377	Homo sapiens	HELI- Human protein sequence SEQ ID NO:12536.	546	61
1873	AAM39099	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2244.	690	77
1873	AAV73467	Homo sapiens	GEMY Human secreted protein clone yd61_1 protein sequence SEQ ID NO:156.	690	77
1873	AAM40885	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 5816.	569	68
1874	gi10121792	Homo sapiens	MJ0495-like protein SelB	2704	99
1874	gi10121790	Mus musculus	MJ0495-like protein SelB	2669	87
1874	gi19354178	Mus musculus	eukaryotic elongation factor, selenocysteine-tRNA-specific	2669	87
1875	AAU20462	Homo sapiens	HUMA- Human secreted protein, Seq ID No 454.	5784	99
1875	AAB94484	Homo sapiens	HELI- Human protein sequence SEQ	4440	99

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Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
			ID NO:15164.		
1875	AAU20467	Homo sapiens	HUMA- Human secreted protein, Seq ID No 459.	3044	98
1876	AAM47798	Homo sapiens	INSP Human RNA helicase RH116.	5309	100
1876	gi12621066	Homo sapiens	RNA helicase-DEAD box protein RH116	5309	100
1876	AAE10155	Homo sapiens	UYCO Human melanoma differentiation associated (Mda)-5 protein.	5285	99
1877	gi4929721	Homo sapiens	CGI-126 protein	777	89
1877	gi6841532	Homo sapiens	HSPC155	772	88
1877	gi18314515	Mus musculus	RIKEN cDNA 1110021H02 gene	760	86
1878	gi2230873	Homo sapiens	M phase phosphoprotein 10	3398	99
1878	AAB34433	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 46 SEQ ID NO:194.	2096	100
1878	gi17944588	Drosophila melanogaster	SD02943p	881	37
1879	gi17861720	Drosophila melanogaster	GH24787p	250	26
1879	gi20343688 ref XP_110124.1	Mus musculus	RIKEN cDNA 3000003F02	820	68
1879	gi21299584 gb EAA11729.1	Anopheles gambiae str. PEST	ebiP4385	228	27
1880	AAM78755	Homo sapiens	HYSE- Human protein SEQ ID NO 1417.	312	75
1880	AAM79739	Homo sapiens	HYSE- Human protein SEQ ID NO 3385.	302	72
1880	gi506502	Mus musculus	NK10	276	68
1881	gi10440371	Homo sapiens	FLJ00020 protein	5999	99
1881	gi18676428	Homo sapiens	FLJ00093 protein	4801	99
1881	gi15077006	Homo sapiens	AT-hook protein AKNA	2452	78
1882	AAB95018	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16726.	778	100
1882	gi17980121	Homo sapiens	BAALC isoform 1-6-8	778	100
1882	gi17979893	Homo sapiens	BAALC 1-6-8	778	100
1883	gi11527289	Homo sapiens	LHX5 protein	2174	100
1883	gi531220	Rattus norvegicus	amino acid feature: homeodomain, bp 895 .. 1074; amino acid feature: LIM1, bp 373 .. 516; amino acid feature: LIM2, bp 550 .. 705	2150	98
1883	gi1388183	Mus musculus	LIM/homeodomain	2150	98
1884	AAG01575	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 5656.	352	82
1885	gi17939572	Homo sapiens	Similar to zinc finger protein 296	2588	100
1885	gi11602755	Mus musculus	zinc finger protein	1216	70
1885	AAU16388	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 1341.	525	59
1886	ABB07493	Homo sapiens	INCY- Human lipid metabolism molecule (LMM) polypeptide (ID: 2965233CD1).	757	99
1886	AAU77498	Homo sapiens	INCY- Human lipid metabolism enzyme, LMM-6.	706	77

Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1886	ABB08205	Homo sapiens	INCY- Human lipid metabolism enzyme-5 (LME-5).	683	77
1887	AAB95718	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18582.	716	100
1887	gi5566262	Chlamydomonas reinhardtii	inner dynein arm I1 intermediate chain IC140	75	28
1887	gi18766204	Plasmodium knowlesi	merozoite surface protein-9 precursor	75	43
1888	gi1542813	Mus musculus	Six5	2908	85
1888	gi11344513	Danio rerio	homeobox protein six4.3	838	37
1888	gi6230605	Homo sapiens	SIX4	812	39
1889	gi19344033	Homo sapiens	similar to pellino (Drosophila) homolog 2	2413	99
1889	gi20810409	Mus musculus	Similar to pellino homolog 2 (Drosophila)	2339	96
1889	AAM93893	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 4027.	1769	100
1890	AAM79760	Homo sapiens	HYSE- Human protein SEQ ID NO 3406.	2825	72
1890	AAM78776	Homo sapiens	HYSE- Human protein SEQ ID NO 1438.	2227	79
1890	gi6467206	Homo sapiens	gonadotropin inducible transcription repressor-4	2063	56
1891	AAM79760	Homo sapiens	HYSE- Human protein SEQ ID NO 3406.	787	78
1891	AAU25446	Homo sapiens	INCY- Human mddt protein from clone LG:1076157.1:2000MAY19.	785	90
1891	AAM78776	Homo sapiens	HYSE- Human protein SEQ ID NO 1438.	713	84
1892	AAU20565	Homo sapiens	HUMA- Human secreted protein, Seq ID No 557.	1891	99
1892	gi6224683	Homo sapiens	unconventional myosin-15	749	34
1892	gi6224685	Mus musculus	unconventional myosin-15	730	33
1893	gi14488277	Homo sapiens	AAT-1 alpha	486	100
1893	gi14488281	Homo sapiens	AAT-1 gamma	152	100
1893	gi14488279	Homo sapiens	AAT-1 beta	152	100
1894	gi14488277	Homo sapiens	AAT-1 alpha	486	100
1894	gi20151303	Drosophila melanogaster	AT22189p	184	21
1894	gi14488281	Homo sapiens	AAT-1 gamma	152	100
1895	gi9963996	Danio rerio	eukaryotic translation initiation factor eIF4E-1	791	75
1895	AAV78505	Homo sapiens	UYMC- Human general translation initiation factor eIF4E amino acid sequence.	775	65
1895	gi849076	Xenopus laevis	eIF-4E protein	775	74
1896	AAB93831	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13650.	1549	100
1896	gi1323281	Saccharomyces cerevisiae	TY2B	83	29
1896	AAV48321	Homo sapiens	META- Human prostate cancer-associated protein 18.	82	31
1897	AAB93831	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13650.	1558	100
1897	gi1323281	Saccharomyces	TY2B	83	29

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Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
		cerevisiae			
1897	gi3249019	Ovis aries	stratifin	81	23
1898	AAB21042	Homo sapiens	INCY- Human nucleic acid-binding protein, NuABP-46.	1016	41
1898	AAM41649	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 6580.	905	40
1898	AAM39863	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 3008.	905	40
1899	gi1339918	Homo sapiens	TR3beta	1778	100
1899	gi1813882	Homo sapiens	DNA binding protein	1585	100
1899	gi292834	Homo sapiens	TR3 orphan receptor	1577	99
1900	gi2276396	Homo sapiens	C2f	1235	100
1900	gi2289907	Mus musculus	C2F	1136	88
1900	gi12805095	Mus musculus	gene rich cluster, C2f gene	1136	88
1901	gi2276396	Homo sapiens	C2f	915	79
1901	gi2289907	Mus musculus	C2F	836	71
1901	gi12805095	Mus musculus	gene rich cluster, C2f gene	836	71
1902	gi2696611	Rattus norvegicus	RNA splicing-related protein	975	84
1902	gi21309836	Trichinella spiralis	glutamic acid-rich protein cNBL1700	165	23
1902	gi9837385	Takifugu rubripes	retinitis pigmentosa GTPase regulator-like protein	161	23
1903	ABB04347	Homo sapiens	SHAN- Human protein phosphatase 4 regulatory subunit 37.	962	99
1903	gi11493267	Homo sapiens	bA196N14.5 (novel protein)	809	100
1903	AAB73355	Homo sapiens	MIYA/ Human mesangial cell meg-1 protein.	503	65
1904	AAW59874	Homo sapiens	HUMA- Amino acid sequence of the cDNA clone CAT-1 (HTXET53).	686	100
1904	AAW08326	Homo sapiens	STRD Human granulysin P522 active fragment.	680	99
1904	AAW08325	Homo sapiens	STRD Human granulysin P520 active fragment.	676	100
1905	AAW08325	Homo sapiens	STRD Human granulysin P520 active fragment.	354	100
1905	AAW59874	Homo sapiens	HUMA- Amino acid sequence of the cDNA clone CAT-1 (HTXET53).	354	100
1905	AAR23732	Homo sapiens	MINU Gene 519 cDNA derived peptide.	354	100
1906	AAW08325	Homo sapiens	STRD Human granulysin P520 active fragment.	327	76
1906	AAW59874	Homo sapiens	HUMA- Amino acid sequence of the cDNA clone CAT-1 (HTXET53).	327	76
1906	AAR23732	Homo sapiens	MINU Gene 519 cDNA derived peptide.	327	76
1907	gi18676436	Homo sapiens	FLJ00102 protein	971	98
1907	gi13569476	Mus musculus	immunity-associated nucleotide 4	359	43
1907	gi18477214	Homo sapiens	human immunity associated protein 1	353	50
1908	AAB94136	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14401.	2885	99
1908	gi15291191	Drosophila melanogaster	GH11140p	1502	52
1908	AAM25505	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1020.	1141	98

Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1909	gi10440532	Homo sapiens	FLJ00116 protein	891	100
1909	gi14211720	Homo sapiens	desmuslin	95	34
1909	gi18698324	Homo sapiens	synemin	88	34
1910	gi10440383	Homo sapiens	FLJ00027 protein	1272	100
1910	gi14336762	Homo sapiens	similar to sperm specific protein	1252	99
1910	gi10801127	Mus musculus	JNK/SAPK-associated protein 1d	1243	97
1911	gi19879663	Homo sapiens	Sam68-like mammalian protein 1	1837	99
1911	gi4426613	Mus musculus	SLM-1	1780	95
1911	gi15824475	Rattus norvegicus	nuclear RNA binding protein SLM-1	1771	95
1912	ABB55747	Homo sapiens	FECH/ Human polypeptide SEQ ID NO 100.	2457	96
1912	AAU39038	Homo sapiens	GEMY Human secreted protein pp392_3.	2457	96
1912	AAY28682	Homo sapiens	GEMY Human pp392_3 secreted protein.	2457	96
1913	gi18150100	Homo sapiens	PKNOX2	2383	100
1913	gi16416147	Homo sapiens	PREP2 protein	2383	100
1913	gi20279043	Mus musculus	homeodomain containing transcription factor PREP2	2347	98
1914	AAB94420	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15022.	4740	100
1914	gi786117	Ensis minor	nuclear protein	169	27
1914	AAM56269	Homo sapiens	MOLE- Human brain expressed single exon probe encoded protein SEQ ID NO: 28374.	158	19
1915	gi8925970	Homo sapiens	eIF4E-transporter	5056	99
1915	gi9857633	Mus musculus	Clast4 protein	4569	89
1915	AAM93322	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 2843.	1532	100
1916	gi8925970	Homo sapiens	eIF4E-transporter	4932	97
1916	gi9857633	Mus musculus	Clast4 protein	4456	88
1916	AAM93322	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 2843.	1408	93
1917	gi2443272	Mus musculus	motor domain of KIF12	611	88
1917	AAB10234	Homo sapiens	GEMY Human fetal brain protein fragment AS32_1i.	516	83
1917	AAW44089	Homo sapiens	GEMY Human secreted protein AS32.	516	83
1918	AAY21622	Homo sapiens	REGC Ligand binding domain of nuclear receptor hMR.	892	84
1918	gi307166	Homo sapiens	mineralocorticoid receptor	892	84
1918	gi15485640	Homo sapiens	mineralocorticoid receptor delta	892	84
1919	gi219931	Homo sapiens	MSS1 protein	922	100
1919	gi1395179	Rattus norvegicus	proteasomal ATPase (MSS1)	922	100
1919	gi12803525	Homo sapiens	proteasome (prosome, macropain) 26S subunit, ATPase, 2	922	100
1920	gi14484930	Mus musculus	DEAQ RNA-dependent ATPase DQX1	1799	78
1920	AAE15259	Homo sapiens	INCY- Human RNA metabolism protein-22 (RMEP-22).	863	41
1920	AAB93069	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11889.	863	41
1921	gi199851gb AAA3975	Mus musculus	pol protein	353	45

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Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
	7.1				
1921	gi 331995 gb AAB03091.1	AKV murine leukemia virus	gag-pol polyprotein (tag amber codon at 2250-2252 inserts Gln in Mo-MuLV)	353	45
1921	gi 927201 gb AAA79247.1	Murine leukemia virus	reverse transcriptase	353	45
1922	gi 2145131 gb AAC45610.1	Streptococcus mutans	repressor of class I heat shock gene expression HrcA	68	32
1923	gi 10862828	Homo sapiens	IFRG15 protein	723	99
1923	gi 10862856	Mus musculus	15kD interferon alpha responsive protein	716	97
1923	AAM49100	Homo sapiens	SHAN- Human peroxisome fatty acid CoA oxidase 14.85.	623	100
1924	AAB43652	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:1097.	565	84
1924	AAB53695	Homo sapiens	HUMA- Human colon cancer antigen protein sequence SEQ ID NO:1235.	565	84
1924	gi495273	Rattus norvegicus	ribosomal protein S15a	565	84
1925	AAG75535	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:6299.	2031	98
1925	gi13397804	Homo sapiens	dJ616B8.3 (novel gene)	458	41
1925	gi13276598	Homo sapiens	dJ614O4.7 (Novel protein)	388	36
1926	AAU16005	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 958.	1802	99
1926	gi55483	Mus musculus	Zfp-1 protein (AA 1-424)	1735	85
1926	gi6467204	Homo sapiens	gonadotropin inducible transcription repressor-3	1079	46
1927	gi16209201	Homo sapiens	keratin 4	1276	55
1927	gi16303309	Mus musculus	type II keratin 5	1273	52
1927	gi3882141	Mus musculus	keratin 6 alpha	1270	52
1928	AAB21000	Homo sapiens	INCY- Human nucleic acid-binding protein, NuABP-4.	1409	100
1928	AAM80207	Homo sapiens	HYSE- Human protein SEQ ID NO 3853.	1354	50
1928	AAM79223	Homo sapiens	HYSE- Human protein SEQ ID NO 1885.	1354	50
1929	AAB95862	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18929.	3435	99
1929	gi10440398	Homo sapiens	FLJ00032 protein	2773	76
1929	gi13752754	Homo sapiens	zinc finger 1111	2631	63
1930	AAB43912	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:1357.	1602	52
1930	AAM79739	Homo sapiens	HYSE- Human protein SEQ ID NO 3385.	1568	40
1930	AAY73346	Homo sapiens	INCY- HTRM clone 619699 protein sequence.	1485	51
1931	gi2564916	Homo sapiens	cotel	85	28
1931	gi2317959	murid herpesvirus 4	tegument protein	78	25
1931	gi6625627	murid herpesvirus 4	64	78	25
1932	AAB92770	Homo sapiens	HELI- Human protein sequence SEQ	441	43

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Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
			ID NO:11245.		
1932	gi15100039	Mus musculus	zinc finger protein ZFEND	441	43
1932	gi498723	Homo sapiens	zinc finger protein	397	42
1933	AAU78843	Homo sapiens	GLAX Human SCAN/KRAB protein associated with a Th2 phenotype (SKAT-2).	4163	99
1933	gi9963806	Homo sapiens	zinc finger protein ZNF287	4142	100
1933	gi11527849	Mus musculus	zinc finger protein SKAT2	3419	82
1934	AAU07883	Homo sapiens	WHED Polypeptide sequence for human hspG1.	1199	68
1934	gi13603873	Homo sapiens	TBP-associated factor II Q	1199	68
1934	gi11877271	Homo sapiens	dJ738A13.1 (similar to TBP (TATA box binding protein))	1089	69
1935	gi3044206	Oryctolagus cuniculus	potassium channel Kv1.5	95	31
1935	gi5932024	Oryctolagus cuniculus	voltage-gated potassium channel Kv1.5	95	31
1935	gi1060973	Oryctolagus cuniculus	Potassium channel	95	31
1936	gi1098934	Mus musculus	Dermo-1	810	100
1936	gi4150892	Rattus norvegicus	dermo-1 protein	810	100
1936	gi17389791	Homo sapiens	dermis expressed 1	810	100
1937	gi13752754	Homo sapiens	zinc finger 1111	2345	58
1937	gi10440398	Homo sapiens	FLJ00032 protein	2290	59
1937	AAB95862	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18929.	2085	59
1938	gi10432400	Homo sapiens	dJ947L8.1.1 (novel CUB and Sushi (SCR repeat) domain protein)	1300	100
1938	AAU11817	Homo sapiens	UYLE- Cancer and neurogenesis associated gene, variant 5R23V2.	1225	58
1938	AAU11816	Homo sapiens	UYLE- Cancer and neurogenesis associated gene, variant 5R-3V2.	1225	58
1939	gi10432400	Homo sapiens	dJ947L8.1.1 (novel CUB and Sushi (SCR repeat) domain protein)	395	95
1939	AAU11817	Homo sapiens	UYLE- Cancer and neurogenesis associated gene, variant 5R23V2.	256	56
1939	AAU11816	Homo sapiens	UYLE- Cancer and neurogenesis associated gene, variant 5R-3V2.	256	56
1940	gi6562077	Homo sapiens	cB33F2.1 (PUTATIVE novel protein similar to C-terminal parts of APOL (apolipoprotein L) and TNF-inducible protein CG12-1)	134	31
1940	gi13384259	Homo sapiens	apolipoprotein L6	134	31
1940	AAO13892	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 27784.	128	32
1941	ABB11454	Homo sapiens	HYSE- Human breast cancer associated Ag homologue, SEQ ID NO:1824.	9267	99
1941	AAU00416	Homo sapiens	ADRE- Human cell regulatory protein p193.	3439	63
1941	AAU15867	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 820.	2310	99
1942	AAB43431	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:876.	869	90

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Table 2B

SEQ ID	Hit ID	Species	Description	S score	Percent identity
1942	gi17932972	Homo sapiens	ribosomal protein S9	869	90
1942	gi12654005	Homo sapiens	Similar to ribosomal protein S9	869	90

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Table 3

SEQ ID	Database entry ID	Description	Results*
972	BL01033	Globins profile.	BL01033A 16.94 3.250e-20 26-47
972	PR00612	ALPHA HAEMOGLOBIN SIGNATURE	PR00612E 9.04 7.000e-19 103-119 PR00612A 8.64 5.800e-14 16-28 PR00612B 10.92 1.000e-13 33-43 PR00612C 12.16 2.286e-13 48-57
972	PR00611	ERYTHROCRUORIN FAMILY SIGNATURE	PR00611A 15.91 5.829e-09 26-48
973	PR00116	ARGINASE SIGNATURE	PR00116D 14.91 4.130e-34 209-238 PR00116B 11.58 9.571e-34 120-147 PR00116A 5.84 1.563e-19 97-112 PR00116E 12.56 7.857e-15 244-258 PR00116C 12.61 2.286e-12 177-195
973	BL00147	Arginase family proteins.	BL00147E 15.08 7.158e-32 208-238 BL00147D 15.27 3.000e-22 120-142 BL00147A 20.22 7.750e-17 10-33 BL00147C 9.48 1.000e-12 97-108 BL00147F 10.93 5.500e-12 252-262 BL00147B 6.88 1.000e-08 49-56
974	PR00116	ARGINASE SIGNATURE	PR00116B 11.58 9.571e-34 120-147 PR00116C 12.61 7.000e-22 177-195 PR00116A 5.84 1.563e-19 97-112 PR00116E 12.56 7.857e-15 244-258 PR00116D 14.91 3.298e-10 209-238
974	BL00147	Arginase family proteins.	BL00147D 15.27 3.000e-22 120-142 BL00147A 20.22 7.750e-17 10-33 BL00147C 9.48 1.000e-12 97-108 BL00147F 10.93 5.500e-12 252-262 BL00147B 6.88 1.000e-08 49-56
975	PR00116	ARGINASE SIGNATURE	PR00116D 14.91 4.130e-34 208-237 PR00116B 11.58 9.571e-34 120-147 PR00116C 12.61 7.000e-22 158-176 PR00116A 5.84 1.563e-19 97-112 PR00116E 12.56 7.857e-15 243-257
975	BL00147	Arginase family proteins.	BL00147E 15.08 7.158e-32 207-237 BL00147D 15.27 3.000e-22 120-142 BL00147A 20.22 7.750e-17 10-33 BL00147C 9.48 1.000e-12 97-108 BL00147F 10.93 5.500e-12 251-261 BL00147B 6.88 1.000e-08 49-56
979	PR00403	WW DOMAIN SIGNATURE	PR00403B 12.19 2.969e-15 307-321
979	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 3.172e-14 307-321
979	BL00297	Heat shock hsp70 proteins family proteins.	BL00297G 21.87 5.358e-09 3-57
980	PR00403	WW DOMAIN SIGNATURE	PR00403B 12.19 2.969e-15 307-321
980	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 3.172e-14 307-321

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Table 3

SEQ ID	Database entry ID	Description	Results*
980	BL00297	Heat shock hsp70 proteins family proteins.	BL00297G 21.87 5.358e-09 3-57
981	BL00031	Nuclear hormones receptors DNA-binding region proteins.	BL00031A 19.55 3.348e-31 11-43 BL00031B 22.25 2.946e-22 45-76
981	PR00398	STEROID HORMONE RECEPTOR SIGNATURE	PR00398A 14.44 7.750e-14 11-28 PR00398C 13.47 8.657e-14 53-71
981	PR00350	VITAMIN D RECEPTOR SIGNATURE	PR00350A 10.48 1.692e-16 11-27 PR00350B 9.35 3.093e-13 28-47
981	PR00047	C4-TYPE STEROID RECEPTOR ZINC FINGER SIGNATURE	PR00047B 7.63 3.348e-17 27-42 PR00047A 15.70 2.200e-16 11-27 PR00047C 5.40 5.000e-10 60-68 PR00047D 13.53 2.607e-09 68-76
983	PF00929	Exonuclease.	PF00929D 16.17 7.366e-09 129-142
986	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 3.636e-11 189-243 PF00791B 28.49 1.413e-09 156-210 PF00791B 28.49 5.128e-09 90-144
986	PF00023	Ank repeat proteins.	PF00023A 16.03 6.571e-11 189-204 PF00023A 16.03 9.571e-11 90-105 PF00023B 14.20 5.500e-09 86-95
986	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 6.870e-09 83-95
987	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.000e-35 10-48
987	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 6.400e-16 541-553 PD00066 13.92 8.200e-16 401-413 PD00066 13.92 8.200e-16 569-581 PD00066 13.92 2.800e-14 513-525 PD00066 13.92 5.200e-14 485-497 PD00066 13.92 7.600e-14 373-385 PD00066 13.92 2.500e-13 457-469 PD00066 13.92 4.000e-13 429-441 PD00066 13.92 8.000e-13 289-301 PD00066 13.92 4.000e-12 261-273 PD00066 13.92 1.391e-11 233-245 PD00066 13.92 8.435e-11 345-357 PD00066 13.92 8.269e-10 317-329
987	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.875e-16 578-591 PR00048A 10.52 3.455e-15 298-311 PR00048A 10.52 4.000e-14 242-255 PR00048A 10.52 9.250e-14 466-479 PR00048A 10.52 1.000e-13 270-283 PR00048A 10.52 2.929e-13 494-507 PR00048A 10.52 3.571e-13 438-451 PR00048A 10.52 8.714e-13 550-563 PR00048A 10.52 9.357e-13 410-423 PR00048A 10.52 6.824e-12 382-395 PR00048A 10.52 7.158e-11 354-367 PR00048B 6.02 7.231e-11 398-407

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Table 3

SEQ ID	Database entry ID	Description	Results*
			PR00048A 10.52 1.000e-10 522-535 PR00048B 6.02 2.688e-10 370-379 PR00048B 6.02 2.688e-10 538-547 PR00048B 6.02 5.500e-10 230-239 PR00048B 6.02 5.500e-10 510-519 PR00048B 6.02 6.625e-10 314-323 PR00048A 10.52 7.261e-10 214-227 PR00048B 6.02 7.750e-10 566-575 PR00048B 6.02 1.474e-09 258-267 PR00048A 10.52 3.520e-09 326-339 PR00048B 6.02 5.737e-09 482-491 PR00048B 6.02 8.579e-09 594-603
987	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.588e-14 301-317 BL00028 16.07 3.647e-14 581-597 BL00028 16.07 2.350e-13 245-261 BL00028 16.07 4.150e-13 469-485 BL00028 16.07 6.850e-13 525-541 BL00028 16.07 2.174e-12 497-513 BL00028 16.07 2.565e-12 413-429 BL00028 16.07 6.087e-12 273-289 BL00028 16.07 9.217e-12 357-373 BL00028 16.07 1.000e-11 385-401 BL00028 16.07 2.731e-11 553-569 BL00028 16.07 4.462e-11 441-457 BL00028 16.07 5.846e-11 217-233 BL00028 16.07 8.971e-09 329-345
990	BL00453	FKBP-type peptidyl-prolyl cis-trans isomerase proteins.	BL00453B 23.86 6.538e-26 222-255 BL00453A 15.57 8.364e-12 190-204
990	PR00280	CHANNEL FORMING COLICIN SIGNATURE	PR00280A 11.09 8.227e-09 225-240
992	BL00750	Chaperonins TCP-1 proteins.	BL00750A 20.07 1.000e-32 23-65 BL00750G 20.12 4.194e-30 386-425 BL00750F 18.40 1.000e-27 325-365 BL00750H 21.44 3.769e-23 443-477 BL00750E 24.59 6.657e-19 251-287 BL00750C 25.65 7.923e-18 100-131 BL00750D 16.16 9.625e-13 150-168
992	PR00304	TAILLESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE	PR00304A 9.20 7.088e-16 32-48 PR00304D 11.04 7.462e-16 328-350 PR00304E 7.79 1.237e-11 362-374 PR00304B 11.60 8.500e-10 54-72
997	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972D 22.55 2.385e-18 1197-1221 BL00972A 11.93 7.120e-18 423-440 BL00972E 20.72 3.250e-13 1223-1244 BL00972C 16.48 4.960e-11 567-581 BL00972B

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Table 3

SEQ ID	Database entry ID	Description	Results*
			9.45 8.269e-10 509-518
1002	PR00219	SYNAPTOBREVIN SIGNATURE	PR00219B 5.46 7.592e-09 383-402
1005	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 4.838e-09 591-639
1006	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 4.838e-09 489-537
1007	BL00037	Myb DNA-binding domain proteins repeat proteins proteins.	BL00037A 16.68 3.571e-11 67-90
1007	PF00569	Zinc finger present in dystrophin, CBP/p300.	PF00569 13.42 4.214e-10 20-36
1008	PR00141	PROTEASOME COMPONENT SIGNATURE	PR00141A 11.36 2.714e-18 80-95 PR00141D 12.45 1.000e-15 290-301 PR00141B 11.15 3.400e-15 254-265 PR00141C 11.15 9.471e-14 265-276
1008	BL00854	Proteasome B-type subunits proteins.	BL00854C 29.92 1.391e-19 237-265 BL00854A 33.93 5.701e-12 77-122 BL00854A 33.93 2.333e-09 130-175 BL00854D 13.76 3.400e-09 288-297
1011	PR00625	DNAJ PROTEIN FAMILY SIGNATURE	PR00625B 13.48 4.309e-10 86-106
1011	BL00636	Nt-dnaJ domain proteins.	BL00636B 15.11 2.756e-09 86-106
1012	DM01782	HYDROGENASE (FE) LARGE CHAIN.	DM01782F 9.01 3.382e-13 320-335 DM01782C 13.88 2.920e-11 173-191 DM01782B 17.29 9.511e-11 118-150
1013	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 6.672e-11 772-786 PR00049D 0.00 1.458e-09 670-684
1013	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.373e-09 591-623 DM00215 19.43 4.814e-09 655-687 DM00215 19.43 6.034e-09 651-683
1013	PR00671	INHIBIN BETA B CHAIN SIGNATURE	PR00671B 4.29 8.105e-09 764-783
1013	PR00021	SMALL PROLINE-RICH PROTEIN SIGNATURE	PR00021B 7.29 8.676e-09 602-611
1014	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 8.615e-14 36-54
1015	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 3.172e-09 664-684
1016	PF00521	DNA gyrase/topoisomerase IV, subunit A.	PF00521G 18.47 7.904e-09 58-91
1017	PF00521	DNA gyrase/topoisomerase IV, subunit A.	PF00521G 18.47 7.904e-09 58-91
1018	BL00227	Tubulin subunits alpha, beta, and gamma proteins.	BL00227B 19.29 1.000e-40 51-105 BL00227C 25.48 1.000e-40 126-177 BL00227D 18.46 1.000e-40 236-289 BL00227F 21.16 3.793e-36 395-448 BL00227A 24.55 2.607e-31 2-35 BL00227E 24.15 2.667e-23 344-378
1019	PF00152	tRNA synthetases class II.	PF00152C 28.03 5.500e-30 390-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			426 PF00152D 21.30 2.161e-29 595-633 PF00152B 15.67 4.414e-16 339-363 PF00152A 19.68 2.552e-15 200-222
1020	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301A 10.24 9.100e-09 65-75
1022	PR00793	PROLYL AMINOPEPTIDASE (S33) FAMILY SIGNATURE	PR00793C 12.24 1.333e-09 142-156
1022	PR00111	ALPHA/BETA HYDROLASE FOLD SIGNATURE	PR00111C 13.46 6.000e-09 156-169
1025	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 7.750e-37 39-77
1025	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.000e-15 316-332 BL00028 16.07 4.600e-13 428-444 BL00028 16.07 6.850e-13 344-360 BL00028 16.07 8.650e-13 372-388 BL00028 16.07 4.130e-12 400-416 BL00028 16.07 6.087e-12 288-304 BL00028 16.07 1.000e-11 232-248 BL00028 16.07 4.808e-11 260-276 BL00028 16.07 5.154e-11 456-472
1025	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.300e-17 304-316 PD00066 13.92 4.462e-15 276-288 PD00066 13.92 4.462e-15 416-428 PD00066 13.92 2.800e-14 388-400 PD00066 13.92 6.143e-12 332-344 PD00066 13.92 7.000e-12 444-456 PD00066 13.92 7.652e-11 248-260 PD00066 13.92 2.500e-09 220-232 PD00066 13.92 4.300e-09 472-484
1025	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 3.250e-14 453-466 PR00048A 10.52 2.929e-13 341-354 PR00048A 10.52 7.429e-13 285-298 PR00048A 10.52 3.118e-12 313-326 PR00048A 10.52 4.176e-12 229-242 PR00048A 10.52 4.176e-12 425-438 PR00048B 6.02 6.000e-12 385-394 PR00048A 10.52 6.824e-12 257-270 PR00048A 10.52 2.421e-11 397-410 PR00048B 6.02 3.077e-11 413-422 PR00048B 6.02 8.615e-11 301-310 PR00048B 6.02 7.188e-10 441-450 PR00048B 6.02 8.875e-10 329-338 PR00048A 10.52 6.400e-09 369-382 PR00048B 6.02 7.158e-09 273-282
1025	PD02462	PROTEIN BOLA TRANSCRIPTION REGULATION AC.	PD02462A 22.48 8.024e-09 393-427
1026	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 8.435e-09 492-504

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Table 3

SEQ ID	Database entry ID	Description	Results*
1030	BL00114	Phosphoribosyl pyrophosphate synthetase proteins.	BL00114D 21.45 8.000e-29 270-320 BL00114B 15.90 7.000e-28 139-184 BL00114A 17.22 2.742e-25 90-136 BL00114E 14.48 9.795e-16 355-378 BL00114C 18.22 5.613e-11 199-233
1032	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 7.032e-09 333-365
1033	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 4.375e-12 305-323
1033	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PD02784C 20.76 5.858e-09 300-345
1034	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 7.000e-10 34-42
1035	PF01062	Putative membrane protein.	PF01062D 18.73 7.882e-25 188-231 PF01062F 17.08 1.960e-22 291-344 PF01062B 15.58 4.343e-16 127-156 PF01062C 15.18 5.269e-11 157-187 PF01062E 16.81 2.182e-09 279-322
1037	BL00048	Protamine P1 proteins.	BL00048 6.39 2.238e-09 83-109
1037	PR00299	ALPHA CRYSTALLIN SIGNATURE	PR00299F 13.20 2.367e-09 220-241
1039	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.800e-12 55-68 PR00019A 11.19 4.000e-09 77-90 PR00019B 11.36 8.560e-09 74-87
1040	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.800e-12 55-68 PR00019A 11.19 4.000e-09 77-90 PR00019B 11.36 8.560e-09 74-87
1042	BL00453	FKBP-type peptidyl-prolyl cis-trans isomerase proteins.	BL00453B 23.86 6.500e-20 232-265
1042	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.568e-09 676-729
1043	PF00043	Glutathione S-transferases.	PF00043 21.83 3.647e-22 36-65
1043	PR00455	TETR BACTERIAL REGULATORY PROTEIN HTH SIGNATURE	PR00455B 17.47 5.227e-09 42-65
1044	PF00043	Glutathione S-transferases.	PF00043 21.83 3.647e-22 54-83
1044	PR00455	TETR BACTERIAL REGULATORY PROTEIN HTH SIGNATURE	PR00455B 17.47 5.227e-09 60-83
1045	PF00043	Glutathione S-transferases.	PF00043 21.83 3.647e-22 54-83
1045	PR00455	TETR BACTERIAL REGULATORY PROTEIN HTH SIGNATURE	PR00455B 17.47 5.227e-09 60-83
1047	BL01162	Quinone oxidoreductase / zeta-crystallin proteins.	BL01162B 18.11 8.163e-18 65-92
1047	BL00059	Zinc-containing alcohol dehydrogenases proteins.	BL00059B 16.08 6.625e-25 65-92 BL00059E 32.37 4.536e-22 155-201 BL00059D 29.23 6.595e-20 104-145 BL00059A 13.36 1.000e-13 34-50
1047	BL00064	L-lactate dehydrogenase proteins.	BL00064A 21.16 9.514e-09 157-194
1047	PR00086	L-LACTATE DEHYDROGENASE SIGNATURE	PR00086A 16.12 9.870e-09 157-181
1049	PR00565	DOPAMINE 1A RECEPTOR	PR00565D 8.94 5.648e-10 222-

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Table 3

SEQ ID	Database entry ID	Description	Results*
		SIGNATURE	240
1050	BL00152	ATP synthase alpha and beta subunits proteins.	BL00152A 15.38 8.147e-09 174-199
1054	PF00731	AIR carboxylase.	PF00731C 23.16 7.333e-35 319-361 PF00731B 19.47 7.429e-28 281-317 PF00731A 19.32 6.333e-24 250-278
1054	BL01057	SAICAR synthetase proteins.	BL01057B 26.96 8.560e-28 31-65 BL01057D 19.84 6.000e-18 114-133 BL01057C 12.89 4.913e-17 93-107 BL01057F 12.94 5.286e-16 185-199 BL01057E 11.12 9.400e-16 166-179 BL01057G 9.73 8.200e-11 206-217 BL01057A 7.65 3.912e-10 16-26
1056	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761E 14.32 1.700e-10 122-140
1061	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.500e-13 191-207 BL00028 16.07 5.500e-13 247-263 BL00028 16.07 8.650e-13 695-711 BL00028 16.07 4.130e-12 275-291 BL00028 16.07 6.087e-12 331-347 BL00028 16.07 6.870e-12 667-683 BL00028 16.07 7.261e-12 611-627 BL00028 16.07 1.346e-11 499-515 BL00028 16.07 2.038e-11 219-235 BL00028 16.07 2.385e-11 555-571 BL00028 16.07 4.462e-11 359-375 BL00028 16.07 4.808e-11 443-459 BL00028 16.07 5.154e-11 471-487 BL00028 16.07 9.308e-11 583-599 BL00028 16.07 1.300e-10 163-179 BL00028 16.07 5.500e-10 639-655 BL00028 16.07 5.500e-10 723-739 BL00028 16.07 6.700e-10 387-403 BL00028 16.07 7.300e-10 303-319
1061	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 4.462e-15 347-359 PD00066 13.92 2.800e-14 207-219 PD00066 13.92 2.800e-14 375-387 PD00066 13.92 5.200e-14 319-331 PD00066 13.92 5.200e-14 599-611 PD00066 13.92 8.800e-14 487-499 PD00066 13.92 1.500e-13 459-471 PD00066 13.92 3.000e-13 683-695 PD00066 13.92 5.000e-13 431-443 PD00066 13.92 6.500e-13 179-191 PD00066 13.92 4.000e-12 235-247 PD00066 13.92 4.429e-12 655-667 PD00066 13.92 4.857e-12 711-723 PD00066 13.92

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Table 3

SEQ ID	Database entry ID	Description	Results*
			9.143e-12 123-135 PD00066 13.92 4.913e-11 403-415 PD00066 13.92 7.261e-11 571-583 PD00066 13.92 7.261e-11 627-639 PD00066 13.92 3.077e-10 291-303 PD00066 13.92 5.846e-10 515-527 PD00066 13.92 7.231e-10 151-163 PD00066 13.92 1.900e-09 263-275
1061	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.750e-14 244-257 PR00048A 10.52 2.929e-13 188-201 PR00048A 10.52 7.429e-13 552-565 PR00048A 10.52 8.714e-13 664-677 PR00048A 10.52 1.529e-12 328-341 PR00048A 10.52 5.235e-12 636-649 PR00048A 10.52 6.824e-12 608-621 PR00048A 10.52 8.412e-12 216-229 PR00048A 10.52 8.941e-12 356-369 PR00048A 10.52 9.471e-12 496-509 PR00048A 10.52 1.000e-11 692-705 PR00048A 10.52 2.421e-11 440-453 PR00048B 6.02 4.462e-11 372-381 PR00048A 10.52 5.737e-11 720-733 PR00048A 10.52 6.211e-11 300-313 PR00048B 6.02 6.538e-11 596-605 PR00048A 10.52 9.526e-11 272-285 PR00048A 10.52 1.000e-10 580-593 PR00048B 6.02 1.563e-10 428-437 PR00048A 10.52 1.783e-10 160-173 PR00048B 6.02 3.250e-10 204-213 PR00048A 10.52 4.522e-10 468-481 PR00048B 6.02 6.063e-10 484-493 PR00048A 10.52 7.652e-10 384-397 PR00048B 6.02 7.750e-10 344-353 PR00048B 6.02 1.947e-09 316-325 PR00048B 6.02 3.842e-09 512-521 PR00048B 6.02 4.789e-09 708-717 PR00048B 6.02 7.158e-09 288-297 PR00048B 6.02 9.053e-09 456-465
1064	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.929e-16 332-348 BL00028 16.07 8.714e-16 668-684 BL00028 16.07 6.824e-14 220-236 BL00028 16.07 7.353e-14 696-712 BL00028 16.07 8.941e-14 360-376 BL00028 16.07 5.500e-13 276-292 BL00028 16.07 1.391e-12 192-208 BL00028 16.07 3.348e-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			12 612-628 BL00028 16.07 4.130e-12 500-516 BL00028 16.07 4.522e-12 304-320 BL00028 16.07 8.043e-12 556- 572 BL00028 16.07 1.000e-11 388-404 BL00028 16.07 1.000e- 11 416-432 BL00028 16.07 4.115e-11 584-600 BL00028 16.07 8.269e-11 752-768 BL00028 16.07 1.300e-10 724- 740 BL00028 16.07 1.600e-10 472-488 BL00028 16.07 3.100e- 10 248-264 BL00028 16.07 3.400e-10 444-460 BL00028 16.07 7.300e-10 528-544 BL00028 16.07 4.857e-09 640- 656
1064	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.545e-15 665- 678 PR00048A 10.52 2.500e-14 329-342 PR00048A 10.52 5.500e-14 553-566 PR00048A 10.52 8.500e-14 217-230 PR00048A 10.52 9.250e-14 497- 510 PR00048A 10.52 2.929e-13 273-286 PR00048A 10.52 2.929e-13 301-314 PR00048A 10.52 4.214e-13 693-706 PR00048A 10.52 5.500e-13 609- 622 PR00048A 10.52 5.500e-13 749-762 PR00048A 10.52 6.143e-13 413-426 PR00048A 10.52 4.176e-12 357-370 PR00048B 6.02 8.000e-12 625- 634 PR00048A 10.52 5.737e-11 385-398 PR00048A 10.52 9.526e-11 189-202 PR00048A 10.52 9.526e-11 525-538 PR00048A 10.52 1.783e-10 721- 734 PR00048B 6.02 3.250e-10 289-298 PR00048B 6.02 3.250e- 10 429-438 PR00048B 6.02 3.813e-10 485-494 PR00048A 10.52 4.522e-10 581-594 PR00048A 10.52 5.696e-10 469- 482 PR00048B 6.02 8.313e-10 513-522 PR00048B 6.02 8.313e- 10 709-718 PR00048B 6.02 8.313e-10 737-746 PR00048A 10.52 9.609e-10 637-650 PR00048B 6.02 1.000e-09 457- 466 PR00048B 6.02 2.895e-09 541-550 PR00048B 6.02 3.842e- 09 569-578 PR00048B 6.02 7.158e-09 261-270 PR00048A 10.52 7.840e-09 245-258 PR00048B 6.02 9.053e-09 597-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			606
1064	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.231e-15 600-612 PD00066 13.92 2.800e-14 292-304 PD00066 13.92 2.800e-14 488-500 PD00066 13.92 2.800e-14 628-640 PD00066 13.92 5.200e-14 544-556 PD00066 13.92 3.000e-13 572-584 PD00066 13.92 3.500e-13 264-276 PD00066 13.92 6.000e-13 208-220 PD00066 13.92 3.143e-12 740-752 PD00066 13.92 3.739e-11 656-668 PD00066 13.92 5.304e-11 320-332 PD00066 13.92 5.304e-11 348-360 PD00066 13.92 5.846e-10 684-696 PD00066 13.92 8.962e-10 516-528 PD00066 13.92 2.200e-09 460-472 PD00066 13.92 3.400e-09 712-724 PD00066 13.92 8.500e-09 376-388 PD00066 13.92 8.500e-09 432-444 PD00066 13.92 9.400e-09 236-248
1069	PR00042	FOS TRANSFORMING PROTEIN SIGNATURE	PR00042D 8.97 6.185e-09 49-70
1070	BL00113	Adenylate kinase proteins.	BL00113A 12.74 3.077e-09 575-591
1070	PR00852	XERODERMA PIGMENTOSUM GROUP D PROTEIN SIGNATURE	PR00852A 11.93 4.638e-09 504-521
1074	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 6.192e-12 13-43
1077	PF01340	Met Apo-repressor, MetJ.	PF01340B 10.11 6.344e-09 914-935
1077	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 6.400e-09 126-138
1077	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.840e-09 135-148
1079	PR00066	XERODERMA PIGMENTOSUM GROUP G PROTEIN SIGNATURE	PR00066A 10.61 6.674e-09 136-153
1082	PR00592	EXTRACELLULAR CALCIUM-SENSING RECEPTOR SIGNATURE	PR00592D 16.76 6.100e-09 2-16
1082	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.	BL00319C 17.12 6.803e-09 102-135
1084	PR00502	MUTT DOMAIN SIGNATURE	PR00502B 15.92 4.643e-09 70-85
1087	BL00977	FAD-dependent glycerol-3-phosphate dehydrogenase proteins.	BL00977A 20.76 9.839e-10 44-95
1089	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.800e-13 250-266 BL00028 16.07 4.600e-13 726-742 BL00028 16.07 6.850e-13 334-350 BL00028 16.07 1.391e-12 502-518 BL00028 16.07 1.391e-12 809-825 BL00028 16.07 4.130e-12 362-378 BL00028 16.07 4.913e-12

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Table 3

SEQ ID	Database entry ID	Description	Results*
			110-126 BL00028 16.07 6.478e-12 222-238 BL00028 16.07 1.692e-11 698-714 BL00028 16.07 3.769e-11 418-434 BL00028 16.07 3.769e-11 614-630 BL00028 16.07 7.231e-11 306-322 BL00028 16.07 7.577e-11 390-406 BL00028 16.07 8.615e-11 446-462 BL00028 16.07 2.200e-10 194-210 BL00028 16.07 2.800e-10 474-490 BL00028 16.07 3.400e-10 670-686 BL00028 16.07 6.100e-10 754-770 BL00028 16.07 8.500e-10 642-658 BL00028 16.07 9.100e-10 138-154 BL00028 16.07 9.100e-10 530-546 BL00028 16.07 1.000e-09 166-182 BL00028 16.07 1.000e-09 558-574 BL00028 16.07 1.257e-09 586-602 BL00028 16.07 4.857e-09 278-294
1089	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 1.000e-14 434-446 PD00066 13.92 8.200e-14 154-166 PD00066 13.92 8.200e-14 210-222 PD00066 13.92 8.200e-14 238-250 PD00066 13.92 8.200e-14 266-278 PD00066 13.92 8.200e-14 350-362 PD00066 13.92 8.200e-14 742-754 PD00066 13.92 3.000e-13 714-726 PD00066 13.92 7.500e-13 322-334 PD00066 13.92 1.000e-12 518-530 PD00066 13.92 1.000e-12 630-642 PD00066 13.92 2.714e-12 602-614 PD00066 13.92 3.143e-12 574-586 PD00066 13.92 5.714e-12 797-809 PD00066 13.92 1.783e-11 686-698 PD00066 13.92 4.522e-11 406-418 PD00066 13.92 7.261e-11 546-558 PD00066 13.92 8.826e-11 490-502 PD00066 13.92 2.385e-10 294-306 PD00066 13.92 5.846e-10 462-474 PD00066 13.92 6.100e-09 770-782 PD00066 13.92 7.300e-09 658-670
1089	BL00245	Phytochrome chromophore attachment site proteins proteins.	BL00245A 10.40 9.000e-09 308-319
1089	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 6.250e-14 331-344 PR00048A 10.52 2.286e-13 247-260 PR00048A 10.52 2.929e-13 219-232 PR00048A 10.52 7.429e-13 275-288

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Table 3

SEQ ID	Database entry ID	Description	Results*
			PR00048A 10.52 8.714e-13 695-708 PR00048A 10.52 1.529e-12 359-372 PR00048B 6.02 8.000e-12 822-831 PR00048A 10.52 1.947e-11 499-512 PR00048A 10.52 5.263e-11 527-540 PR00048A 10.52 6.684e-11 806-819 PR00048A 10.52 7.158e-11 415-428 PR00048A 10.52 1.391e-10 751-764 PR00048A 10.52 2.174e-10 303-316 PR00048A 10.52 2.174e-10 387-400 PR00048B 6.02 3.250e-10 151-160 PR00048B 6.02 3.250e-10 235-244 PR00048B 6.02 3.250e-10 263-272 PR00048B 6.02 3.250e-10 739-748 PR00048A 10.52 3.348e-10 191-204 PR00048A 10.52 3.348e-10 723-736 PR00048A 10.52 4.130e-10 443-456 PR00048A 10.52 4.913e-10 667-680 PR00048B 6.02 4.938e-10 515-524 PR00048B 6.02 4.938e-10 627-636 PR00048A 10.52 7.261e-10 471-484 PR00048B 6.02 8.313e-10 347-356 PR00048B 6.02 8.313e-10 711-720 PR00048A 10.52 8.826e-10 163-176 PR00048A 10.52 9.217e-10 639-652 PR00048B 6.02 1.947e-09 207-216 PR00048B 6.02 1.947e-09 794-803 PR00048A 10.52 2.800e-09 555-568 PR00048A 10.52 4.600e-09 135-148 PR00048B 6.02 7.158e-09 431-440 PR00048A 10.52 8.560e-09 583-596 PR00048B 6.02 1.000e-08 487-496
1093	BL00292	Cyclins proteins.	BL00292A 22.87 6.786e-24 178-211 BL00292B 20.31 3.739e-19 221-251
1094	BL00752	XPA protein.	BL00752B 19.17 6.289e-09 542-585
1095	BL00495	Apple domain proteins.	BL00495E 14.56 8.065e-09 527-563
1096	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456F 5.86 5.219e-10 122-133
1103	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.545e-11 217-230
1105	BL00845	CAP-Gly domain proteins.	BL00845 16.43 6.538e-26 155-179
1105	BL00299	Ubiquitin domain proteins.	BL00299 28.84 9.813e-19 27-78
1106	BL00660	Band 4.1 family domain proteins.	BL00660B 17.33 4.375e-30 189-228 BL00660C 23.36 7.811e-30

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Table 3

SEQ ID	Database entry ID	Description	Results*
			268-311 BL00660A 31.50 3.854e-29 106-158 BL00660E 23.41 1.818e-19 352-374 BL00660D 13.60 8.147e-18 319-342
1106	PR00935	BAND 4.1 PROTEIN FAMILY SIGNATURE	PR00935C 11.98 8.579e-21 207-227 PR00935D 10.20 7.750e-14 268-284 PR00935B 10.58 9.419e-13 194-207 PR00935A 10.16 1.563e-11 130-142
1106	PR00661	ERM FAMILY SIGNATURE	PR00661C 9.53 2.600e-09 203-224
1107	BL00660	Band 4.1 family domain proteins.	BL00660B 17.33 4.375e-30 189-228 BL00660C 23.36 7.811e-30 268-311 BL00660A 31.50 3.854e-29 106-158 BL00660E 23.41 1.818e-19 352-374 BL00660D 13.60 8.147e-18 319-342
1107	PR00935	BAND 4.1 PROTEIN FAMILY SIGNATURE	PR00935C 11.98 8.579e-21 207-227 PR00935D 10.20 7.750e-14 268-284 PR00935B 10.58 9.419e-13 194-207 PR00935A 10.16 1.563e-11 130-142
1107	PR00661	ERM FAMILY SIGNATURE	PR00661C 9.53 2.600e-09 203-224
1108	PD02059	CORE POLYPROTEIN PROTEIN GAG CONTAINS: P.	PD02059B 24.48 1.634e-09 590-624 PD02059B 24.48 1.634e-09 595-629
1108	BL00415	Synapsins proteins.	BL00415N 4.29 5.861e-09 610-653
1108	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.143e-14 602-634 DM00215 19.43 6.571e-14 598-630 DM00215 19.43 9.786e-14 600-632 DM00215 19.43 9.413e-13 593-625 DM00215 19.43 5.313e-12 594-626 DM00215 19.43 6.625e-12 596-628 DM00215 19.43 2.059e-11 597-629 DM00215 19.43 2.235e-11 592-624 DM00215 19.43 4.375e-10 595-627 DM00215 19.43 4.857e-10 603-635 DM00215 19.43 5.982e-10 605-637 DM00215 19.43 9.196e-10 608-640 DM00215 19.43 5.119e-09 580-612 DM00215 19.43 6.949e-09 612-644 DM00215 19.43 8.780e-09 607-639
1108	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.714e-11 599-613 PR00049D 0.00 8.941e-11 616-630 PR00049D 0.00 1.286e-10 601-615 PR00049D 0.00 1.714e-10 600-614 PR00049D 0.00 4.071e-10 609-623 PR00049D 0.00 8.786e-10 598-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			612 PR00049D 0.00 3.746e-09 602-616 PR00049D 0.00 4.966e-09 615-629 PR00049D 0.00 6.186e-09 608-622 PR00049D 0.00 6.186e-09 610-624 PR00049D 0.00 6.186e-09 612-626 PR00049D 0.00 7.102e-09 614-628 PR00049D 0.00 9.390e-09 618-632
1108	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 1.276e-11 606-626 PR00211B 0.86 7.796e-11 612-632 PR00211B 0.86 6.452e-10 610-630 PR00211B 0.86 9.417e-09 605-625
1110	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 1.783e-11 436-450 PR00320A 16.74 6.897e-11 436-450 PR00320B 12.19 3.057e-10 436-450
1110	PR00962	LETHAL(2) GIANT LARVAE PROTEIN SIGNATURE	PR00962D 10.40 4.433e-09 433-456
1111	BL00795	Involucrin proteins.	BL00795C 17.06 3.900e-09 57-101
1115	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 8.642e-26 9-47
1115	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 1.000e-15 241-253 PD00066 13.92 3.077e-15 409-421 PD00066 13.92 3.077e-15 437-449 PD00066 13.92 2.800e-14 465-477 PD00066 13.92 5.800e-14 381-393 PD00066 13.92 3.143e-12 297-309 PD00066 13.92 7.857e-12 213-225 PD00066 13.92 8.286e-12 325-337 PD00066 13.92 4.462e-10 353-365
1115	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 6.824e-14 253-269 BL00028 16.07 1.450e-13 393-409 BL00028 16.07 5.500e-13 197-213 BL00028 16.07 3.348e-12 449-465 BL00028 16.07 6.478e-12 337-353 BL00028 16.07 8.826e-12 365-381 BL00028 16.07 9.609e-12 421-437 BL00028 16.07 3.769e-11 477-493 BL00028 16.07 1.000e-10 225-241 BL00028 16.07 1.000e-10 281-297 BL00028 16.07 5.800e-10 309-325
1115	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 1.000e-13 446-459 PR00048A 10.52 8.071e-13 334-347 PR00048A 10.52 2.588e-12 390-403 PR00048A 10.52 2.588e-12 418-431 PR00048A 10.52 7.882e-12 250-263 PR00048B 6.02 1.000e-11

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Table 3

SEQ ID	Database entry ID	Description	Results*
			406-415 PR00048B 6.02 1.000e-11 434-443 PR00048A 10.52 2.421e-11 474-487 PR00048B 6.02 3.769e-11 238-247 PR00048B 6.02 6.538e-11 378-387 PR00048A 10.52 1.391e-10 362-375 PR00048A 10.52 2.565e-10 222-235 PR00048A 10.52 4.522e-10 306-319 PR00048B 6.02 2.421e-09 210-219 PR00048B 6.02 4.316e-09 294-303 PR00048B 6.02 4.316e-09 322-331 PR00048B 6.02 7.158e-09 490-499
1115	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970A 8.50 7.750e-09 196-202
1116	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 8.615e-10 345-354 DM00099B 14.73 4.375e-09 439-448
1117	BL01282	BIR repeat proteins.	BL01282B 30.49 1.136e-10 273-311
1118	PR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245C 7.84 7.500e-12 40-55
1118	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.059e-14 478-494 BL00028 16.07 6.400e-13 506-522 BL00028 16.07 1.692e-11 426-442 BL00028 16.07 2.038e-11 398-414 BL00028 16.07 5.500e-11 370-386
1118	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.800e-14 386-398 PD00066 13.92 2.385e-10 494-506
1118	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 9.550e-10 215-253
1118	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.043e-10 367-380 PR00048B 6.02 1.000e-09 383-392 PR00048A 10.52 5.320e-09 503-516 PR00048A 10.52 6.760e-09 395-408
1119	PR00679	PROHIBITIN SIGNATURE	PR00679F 8.03 6.478e-28 207-230 PR00679C 14.44 7.677e-22 136-154 PR00679B 13.63 6.769e-20 113-132 PR00679E 12.82 5.171e-19 182-201 PR00679D 11.91 9.053e-18 159-175 PR00679G 6.13 7.882e-17 230-246
1122	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.800e-14 243-255 PD00066 13.92 2.800e-14 467-479 PD00066 13.92 5.800e-14 383-395 PD00066 13.92 9.400e-14 299-311 PD00066 13.92 1.500e-13 355-367 PD00066 13.92 2.500e-13 159-171 PD00066 13.92 2.500e-13 411-423 PD00066 13.92 5.000e-13 327-339 PD00066 13.92

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Table 3

SEQ ID	Database entry ID	Description	Results*
			6.143e-12 215-227 PD00066 13.92 2.565e-11 187-199 PD00066 13.92 7.261e-11 439-451
1122	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.000e-15 479-495 BL00028 16.07 6.294e-14 283-299 BL00028 16.07 8.412e-14 143-159 BL00028 16.07 3.250e-13 199-215 BL00028 16.07 4.150e-13 395-411 BL00028 16.07 2.957e-12 171-187 BL00028 16.07 3.348e-12 311-327 BL00028 16.07 8.435e-12 451-467 BL00028 16.07 1.692e-11 227-243 BL00028 16.07 2.038e-11 255-271 BL00028 16.07 3.700e-10 367-383 BL00028 16.07 5.200e-10 339-355
1122	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 6.625e-16 224-237 PR00048A 10.52 9.250e-14 476-489 PR00048A 10.52 1.643e-13 196-209 PR00048A 10.52 2.059e-12 392-405 PR00048A 10.52 3.647e-12 140-153 PR00048B 6.02 6.000e-12 324-333 PR00048A 10.52 6.294e-12 336-349 PR00048A 10.52 7.353e-12 252-265 PR00048A 10.52 7.882e-12 448-461 PR00048A 10.52 1.947e-11 168-181 PR00048A 10.52 1.947e-11 280-293 PR00048A 10.52 3.368e-11 308-321 PR00048B 6.02 7.923e-11 296-305 PR00048B 6.02 1.563e-10 408-417 PR00048A 10.52 1.783e-10 364-377 PR00048B 6.02 3.250e-10 240-249 PR00048B 6.02 5.500e-10 464-473 PR00048B 6.02 1.947e-09 380-389 PR00048B 6.02 2.421e-09 268-277 PR00048B 6.02 4.789e-09 184-193 PR00048B 6.02 6.684e-09 212-221 PR00048B 6.02 8.579e-09 156-165
1122	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479A 19.86 5.610e-10 214-236 BL00479A 19.86 9.809e-09 354-376
1124	PR00987	GLUTAMYL-TRNA SYNTHETASE SIGNATURE	PR00987A 12.14 1.794e-14 40-52 PR00987D 12.77 3.520e-12 226-236 PR00987C 9.71 5.263e-12 69-82 PR00987B 7.26 3.829e-11 54-65 PR00987E 12.13 7.975e-09 242-250

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Table 3

SEQ ID	Database entry ID	Description	Results*
1126	BL00226	Intermediate filaments proteins.	BL00226D 19.10 5.821e-10 856-902
1126	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972D 22.55 4.194e-16 89-113 BL00972E 20.72 6.897e-10 122-143
1126	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761E 14.32 7.063e-09 428-446
1128	BL00034	'Paired box' domain proteins.	BL00034A 11.69 1.000e-40 74-124 BL00034B 12.33 3.750e-34 128-164 BL00034C 14.82 8.200e-34 168-198
1128	PR00027	PAIRED BOX SIGNATURE	PR00027C 10.36 7.088e-22 116-133 PR00027B 15.39 5.629e-21 96-114 PR00027A 8.97 1.346e-20 78-93 PR00027D 3.72 5.821e-20 134-151
1129	PF00624	Flocculin repeat proteins.	PF00624I 9.10 5.748e-09 314-343
1137	PR00838	VENOM ALLERGEN 5 SIGNATURE	PR00838G 16.07 2.080e-12 74-93
1137	PR00837	ALLERGEN V5/TPX-1 FAMILY SIGNATURE	PR00837C 17.21 2.588e-10 75-91 PR00837D 11.12 6.023e-09 102-115
1137	BL01009	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins.	BL01009B 13.88 1.000e-12 62-73 BL01009D 14.19 8.293e-12 76-96 BL01009E 13.50 8.642e-09 101-116
1139	BL01172	Ribosomal protein L44e proteins.	BL01172B 14.10 9.270e-36 15-56 BL01172C 16.78 3.455e-27 63-101 BL01172A 7.78 4.600e-12 2-12
1141	BL00625	Regulator of chromosome condensation (RCC1) proteins.	BL00625A 16.21 3.951e-16 166-194 BL00625A 16.21 1.138e-15 218-246 BL00625A 16.21 4.296e-13 308-336 BL00625B 17.69 2.479e-12 212-245 BL00625B 17.69 6.301e-12 160-193 BL00625B 17.69 7.288e-12 302-335
1141	PR00597	GELSOLIN FAMILY SIGNATURE	PR00597G 8.55 5.291e-09 162-184
1141	PR00633	CHROMOSOME CONDENSATION REGULATOR RCC1 SIGNATURE	PR00633F 10.03 5.671e-09 321-335 PR00633G 13.71 6.000e-09 218-236 PR00633H 15.10 8.573e-09 172-193 PR00633A 9.32 8.597e-09 178-194
1145	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 7.722e-09 23-42
1148	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 3.394e-09 581-635
1148	BL00276	Channel forming colicins proteins.	BL00276A 8.87 6.750e-09 375-386
1149	BL00598	Chromo domain proteins.	BL00598 14.45 6.250e-20 28-49
1149	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE	PR00929C 5.26 7.341e-11 72-82 PR00929A 3.25 4.927e-10 74-84 PR00929B 4.38 8.380e-10 72-83
1149	BL00354	HMG-I and HMG-Y DNA-binding domain	BL00354B 3.16 3.959e-10 71-83

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Table 3

SEQ ID	Database entry ID	Description	Results*
		proteins (A+T-hook).	BL00354A 3.83 1.270e-09 74-83
1149	PR00504	CHROMODOMAIN SIGNATURE	PR00504B 9.12 2.853e-12 22-36 PR00504C 11.19 2.102e-09 37-49
1152	BL00113	Adenylate kinase proteins.	BL00113A 12.74 8.615e-09 247-263
1153	BL00019	Actinin-type actin-binding domain proteins.	BL00019D 15.33 8.740e-17 21-50
1153	BL00478	LIM domain proteins.	BL00478B 14.79 1.000e-12 184-198
1156	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 7.000e-12 253-265 BL00018 7.41 9.217e-09 294-306
1161	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 1.000e-14 402-414 PD00066 13.92 1.000e-13 458-470 PD00066 13.92 9.500e-13 430-442
1161	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 6.870e-12 414-430 BL00028 16.07 5.154e-11 358-374 BL00028 16.07 1.000e-10 470-486 BL00028 16.07 5.800e-10 386-402 BL00028 16.07 5.800e-10 442-458
1161	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 6.211e-11 467-480 PR00048A 10.52 3.348e-10 411-424 PR00048A 10.52 1.360e-09 355-368 PR00048B 6.02 1.947e-09 455-464 PR00048A 10.52 2.440e-09 439-452 PR00048B 6.02 2.895e-09 427-436 PR00048B 6.02 3.842e-09 399-408
1161	BL00034	'Paired box' domain proteins.	BL00034D 7.94 9.308e-09 335-345
1162	BL01113	C1q domain proteins.	BL01113B 18.26 5.421e-16 383-418
1162	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007A 19.33 8.568e-14 377-403
1163	BL00674	AAA-protein family proteins.	BL00674B 4.46 8.714e-10 26-47
1163	PR00051	BACTERIAL CHROMOSOMAL REPLICATION INITIATOR (DNAA) SIGNATURE	PR00051A 10.68 4.843e-09 26-46
1163	BL01008	DnaA protein.	BL01008B 12.53 7.609e-09 26-40
1164	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380D 9.93 1.931e-21 305-326 PR00380A 14.18 1.659e-20 104-125 PR00380B 12.64 8.962e-17 219-236 PR00380C 13.18 2.500e-15 253-271
1164	BL00411	Kinesin motor domain proteins.	BL00411G 21.39 3.160e-31 254-295 BL00411H 15.66 2.125e-28 304-334 BL00411C 15.04 6.000e-22 104-125 BL00411F 14.77 7.545e-19 210-234 BL00411E 10.43 7.279e-13 153-171 BL00411A 11.31 7.387e-11 11-25 BL00411B 13.51 2.969e-10 70-86
1168	PR00910	LUTEOVIRUS ORF6 PROTEIN	PR00910A 2.51 6.704e-12 490-

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Table 3

SEQ ID	Database entry ID	Description	Results*
		SIGNATURE	502 PR00910A 2.51 8.986e-12 498-510 PR00910A 2.51 5.315e-11 494-506 PR00910A 2.51 6.671e-11 486-498 PR00910A 2.51 1.667e-10 492-504 PR00910A 2.51 3.778e-10 482-494 PR00910A 2.51 1.214e-09 484-496 PR00910A 2.51 3.250e-09 496-508 PR00910A 2.51 6.571e-09 488-500
1169	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 3.063e-28 16-54
1172	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.200e-30 25-63
1172	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 8.313e-15 244-260 BL00028 16.07 3.250e-13 216-232 BL00028 16.07 3.250e-13 272-288 BL00028 16.07 5.304e-12 160-176 BL00028 16.07 5.696e-12 328-344 BL00028 16.07 4.462e-11 300-316 BL00028 16.07 6.885e-11 188-204 BL00028 16.07 4.000e-10 356-372
1172	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.846e-15 232-244 PD00066 13.92 7.923e-15 344-356 PD00066 13.92 2.800e-14 316-328 PD00066 13.92 7.600e-14 204-216 PD00066 13.92 1.500e-13 288-300 PD00066 13.92 5.154e-10 176-188 PD00066 13.92 3.400e-09 260-272
1172	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 1.000e-15 213-226 PR00048A 10.52 9.250e-14 241-254 PR00048B 6.02 6.400e-13 313-322 PR00048A 10.52 8.071e-13 157-170 PR00048A 10.52 7.882e-12 325-338 PR00048B 6.02 2.385e-11 201-210 PR00048A 10.52 2.421e-11 185-198 PR00048B 6.02 3.769e-11 341-350 PR00048B 6.02 7.231e-11 257-266 PR00048A 10.52 1.391e-10 353-366 PR00048B 6.02 2.688e-10 229-238 PR00048A 10.52 4.522e-10 297-310 PR00048B 6.02 1.947e-09 285-294 PR00048A 10.52 6.040e-09 269-282
1173	PR00502	MUTT DOMAIN SIGNATURE	PR00502B 15.92 4.643e-09 70-85
1174	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 4.706e-12 45-58 PR00048B 6.02 8.000e-12 33-42
1174	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.200e-14 36-48 PD00066 13.92 5.154e-10 8-20
1174	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.654e-11 48-64

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Table 3

SEQ ID	Database entry ID	Description	Results*
			BL00028 16.07 3.829e-09 20-36
1176	PR00401	SH2 DOMAIN SIGNATURE	PR00401E 14.10 5.179e-10 119-133
1179	PF01105	emp24/gp25L/p24 family.	PF01105B 25.12 2.016e-20 72-123
1180	PR00452	SH3 DOMAIN SIGNATURE	PR00452D 17.02 4.462e-09 561-573
1181	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 5.146e-11 88-102 PR00456E 3.06 9.063e-10 89-103 PR00456E 3.06 9.156e-10 87-101
1181	BL00795	Involucrin proteins.	BL00795C 17.06 1.200e-09 107-151
1181	BL00826	MARCKS family proteins.	BL00826C 7.63 8.313e-09 94-120
1181	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 5.899e-10 84-98 PR00308A 5.90 8.405e-10 88-102 PR00308C 3.83 8.892e-10 88-97 PR00308C 3.83 8.892e-10 89-98 PR00308C 3.83 8.892e-10 90-99 PR00308C 3.83 8.892e-10 91-100 PR00308C 3.83 8.892e-10 92-101 PR00308C 3.83 8.892e-10 93-102 PR00308C 3.83 8.892e-10 153-162 PR00308C 3.83 8.892e-10 154-163 PR00308C 3.83 8.892e-10 155-164 PR00308A 5.90 9.772e-10 87-101 PR00308A 5.90 3.541e-09 89-103 PR00308A 5.90 3.647e-09 150-164 PR00308C 3.83 7.545e-09 152-161 PR00308C 3.83 8.831e-09 87-96
1181	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	PR00208A 12.59 6.294e-10 103-120 PR00208A 12.59 6.294e-10 104-121 PR00208A 12.59 6.294e-10 105-122 PR00208A 12.59 6.294e-10 106-123 PR00208A 12.59 6.294e-10 107-124 PR00208A 12.59 6.294e-10 108-125 PR00208A 12.59 6.294e-10 109-126 PR00208A 12.59 6.294e-10 110-127 PR00208A 12.59 6.426e-10 112-129 PR00208A 12.59 7.750e-10 114-131 PR00208A 12.59 2.110e-09 111-128 PR00208A 12.59 7.904e-09 102-119 PR00208A 12.59 8.274e-09 113-130 PR00208A 12.59 9.014e-09 117-134
1181	PR00833	POLLEN ALLERGEN POA PI SIGNATURE	PR00833H 2.30 3.192e-09 88-102 PR00833D 8.66 9.900e-09 155-172
1184	BL00406	Actins proteins.	BL00406C 6.75 3.629e-11 271-325 BL00406A 9.95 1.000e-09 48-82 BL00406E 8.44 7.070e-09 572-621

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Table 3

SEQ ID	Database entry ID	Description	Results*
1185	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 5.404e-09 526-549
1185	DM01688	2 POLY-IG RECEPTOR.	DM01688I 14.97 8.615e-09 1902-1949
1186	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 5.000e-17 1191-1203
1186	BL00326	Tropomyosins proteins.	BL00326B 7.68 9.061e-09 901-949
1186	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.382e-12 490-543 BL01160B 19.54 2.850e-11 483-536 BL01160B 19.54 6.676e-10 781-834 BL01160B 19.54 9.390e-09 497-550
1188	PR00613	MYOGLOBIN SIGNATURE	PR00613F 7.87 1.529e-31 136-165 PR00613B 9.02 8.200e-31 38-61 PR00613C 10.22 7.545e-25 71-91 PR00613E 9.09 4.000e-24 110-130 PR00613D 9.83 7.353e-23 92-109 PR00613A 8.32 4.600e-20 19-33
1188	BL01033	Globins profile.	BL01033A 16.94 1.500e-14 38-59
1188	PR00611	ERYTHROCRUORIN FAMILY SIGNATURE	PR00611A 15.91 5.829e-09 38-60
1190	BL01266	Adenylosuccinate synthetase GTP-binding site proteins.	BL01266E 20.85 1.000e-40 326-367 BL01266D 15.21 4.000e-40 250-288 BL01266A 18.16 5.500e-39 40-78 BL01266C 15.30 4.115e-26 160-185 BL01266F 22.92 3.250e-21 422-450 BL01266B 13.74 2.421e-20 127-146
1191	PR00625	DNAJ PROTEIN FAMILY SIGNATURE	PR00625D 11.93 4.692e-09 444-454
1192	PR00460	BACTERIAL HAEM CATALASE-PEROXIDASE SIGNATURE	PR00460K 10.79 6.835e-09 1535-1564
1193	BL01162	Quinone oxidoreductase / zeta-crystallin proteins.	BL01162C 22.80 4.429e-30 167-210 BL01162B 18.11 4.977e-20 107-134 BL01162A 15.38 1.844e-12 78-100
1193	BL00059	Zinc-containing alcohol dehydrogenases proteins.	BL00059B 16.08 3.250e-16 107-134 BL00059D 29.23 5.563e-09 136-177
1202	PF00646	F-box domain proteins.	PF00646A 14.37 4.536e-10 676-689
1204	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.652e-11 32-44 PD00066 13.92 8.826e-11 60-72 PD00066 13.92 2.731e-10 4-16 PD00066 13.92 5.846e-10 90-102
1204	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.500e-13 44-60 BL00028 16.07 8.269e-11 16-32 BL00028 16.07 4.900e-10 132-148 BL00028 16.07 8.800e-10 74-90 BL00028 16.07 5.371e-09 102-118
1204	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 1.000e-10 41-54

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Table 3

SEQ ID	Database entry ID	Description	Results*
			PR00048A 10.52 1.391e-10 13-26 PR00048B 6.02 1.947e-09 57-66 PR00048A 10.52 8.560e-09 71-84
1205	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 5.286e-10 50-58
1207	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 5.765e-11 315-347 DM00215 19.43 5.941e-11 311-343 DM00215 19.43 3.411e-10 310-342 DM00215 19.43 9.518e-10 309-341 DM00215 19.43 1.763e-09 281-313 DM00215 19.43 6.949e-09 300-332 DM00215 19.43 8.322e-09 287-319
1207	PD02059	CORE POLYPROTEIN PROTEIN GAG CONTAINS: P.	PD02059B 24.48 8.352e-09 297-331
1207	PF00992	Troponin.	PF00992A 16.67 8.816e-09 452-486
1207	PF01140	Matrix protein (MA), p15.	PF01140D 15.54 2.320e-11 405-439 PF01140D 15.54 9.686e-09 393-427
1207	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 6.602e-11 305-325 PR00211B 0.86 6.106e-10 299-319 PR00211B 0.86 3.167e-09 312-332 PR00211B 0.86 9.917e-09 318-338
1212	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 4.300e-10 289-305 BL00028 16.07 4.600e-10 620-636 BL00028 16.07 4.900e-10 361-377 BL00028 16.07 7.600e-10 488-504 BL00028 16.07 2.286e-09 232-248
1219	PF00569	Zinc finger present in dystrophin, CBP/p300.	PF00569 13.42 3.182e-16 55-71
1220	BL00422	Granins proteins.	BL00422C 16.18 7.136e-11 543-570
1220	BL00824	Elongation factor 1 beta/beta'/delta chain proteins.	BL00824B 9.21 8.176e-09 540-559
1224	PD02448	TRANSCRIPTION PROTEIN DNA-BINDIN.	PD02448A 9.37 4.585e-09 86-124
1225	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.750e-15 353-369 BL00028 16.07 7.750e-15 465-481 BL00028 16.07 1.529e-14 381-397 BL00028 16.07 2.059e-14 325-341 BL00028 16.07 7.882e-14 437-453 BL00028 16.07 6.850e-13 409-425 BL00028 16.07 1.346e-11 297-313 BL00028 16.07 2.385e-11 493-509
1225	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 2.636e-15 378-391 PR00048A 10.52 5.909e-15 406-419 PR00048A 10.52 7.545e-15 462-475 PR00048A 10.52 1.000e-13 434-447

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Table 3

SEQ ID	Database entry ID	Description	Results*
			PR00048A 10.52 2.929e-13 350-363 PR00048A 10.52 5.765e-12 294-307 PR00048A 10.52 5.765e-12 322-335 PR00048B 6.02 6.000e-12 394-403 PR00048B 6.02 1.000e-11 282-291 PR00048A 10.52 5.263e-11 490-503 PR00048B 6.02 3.250e-10 450-459 PR00048B 6.02 4.375e-10 338-347 PR00048B 6.02 5.500e-10 366-375 PR00048B 6.02 1.947e-09 422-431 PR00048B 6.02 6.211e-09 478-487 PR00048B 6.02 7.158e-09 310-319
1225	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.800e-14 285-297 PD00066 13.92 2.800e-14 369-381 PD00066 13.92 1.000e-13 425-437 PD00066 13.92 5.500e-13 397-409 PD00066 13.92 4.000e-12 453-465 PD00066 13.92 7.261e-11 313-325 PD00066 13.92 8.800e-09 481-493
1229	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 4.558e-31 10-48
1229	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.438e-15 357-373 BL00028 16.07 2.174e-12 161-177 BL00028 16.07 2.957e-12 189-205 BL00028 16.07 1.346e-11 329-345 BL00028 16.07 2.385e-11 273-289 BL00028 16.07 5.846e-11 217-233 BL00028 16.07 7.600e-10 245-261 BL00028 16.07 2.029e-09 301-317
1229	PD02462	PROTEIN BOLA TRANSCRIPTION REGULATION AC.	PD02462A 22.48 3.524e-09 294-328
1229	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.846e-15 317-329 PD00066 13.92 7.231e-15 233-245 PD00066 13.92 3.000e-13 289-301 PD00066 13.92 7.000e-13 345-357 PD00066 13.92 5.500e-09 177-189 PD00066 13.92 6.400e-09 205-217
1229	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 2.059e-12 186-199 PR00048A 10.52 3.118e-12 214-227 PR00048A 10.52 5.765e-12 354-367 PR00048A 10.52 8.412e-12 326-339 PR00048A 10.52 8.941e-12 158-171 PR00048A 10.52 2.895e-11 242-255 PR00048A 10.52 2.565e-10 298-311 PR00048A 10.52 2.957e-10 270-283

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Table 3

SEQ ID	Database entry ID	Description	Results*
			PR00048B 6.02 4.938e-10 314-323 PR00048B 6.02 8.105e-09 342-351
1230	BL00478	LIM domain proteins.	BL00478B 14.79 8.435e-14 26-40
1230	PR00510	NEBULIN SIGNATURE	PR00510C 14.84 2.662e-14 513-532 PR00510D 9.21 7.261e-11 534-549 PR00510E 14.55 6.425e-10 552-570 PR00510D 9.21 3.165e-09 321-336 PR00510A 9.09 7.223e-09 219-238
1232	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.373e-09 451-483
1236	PF00901	Orbivirus outer capsid protein VP5.	PF00901D 19.87 8.579e-09 220-274
1236	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 9.667e-09 42-50
1238	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 8.800e-15 18-42 BL00215A 15.82 2.071e-12 212-236 BL00215A 15.82 3.571e-12 114-138 BL00215B 10.44 9.526e-11 63-75 BL00215B 10.44 1.600e-09 257-269
1243	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.588e-14 725-741
1243	BL00415	Synapsins proteins.	BL00415P 2.37 3.483e-09 19-54
1243	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 3.520e-09 722-735
1247	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 3.647e-14 349-365 BL00028 16.07 8.941e-14 153-169 BL00028 16.07 2.800e-13 237-253 BL00028 16.07 6.850e-13 181-197 BL00028 16.07 2.174e-12 433-449 BL00028 16.07 2.957e-12 321-337 BL00028 16.07 1.692e-11 209-225 BL00028 16.07 1.692e-11 405-421 BL00028 16.07 2.038e-11 265-281 BL00028 16.07 4.462e-11 293-309 BL00028 16.07 4.808e-11 461-477 BL00028 16.07 3.100e-10 377-393
1247	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 1.900e-16 197-209 PD00066 13.92 6.400e-16 253-265 PD00066 13.92 1.600e-14 449-461 PD00066 13.92 4.600e-14 225-237 PD00066 13.92 7.000e-14 169-181 PD00066 13.92 5.500e-13 393-405 PD00066 13.92 8.000e-13 281-293 PD00066 13.92 8.500e-13 309-321 PD00066 13.92 8.500e-13 365-377 PD00066 13.92 4.429e-12 337-349 PD00066 13.92 3.423e-10 421-433

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Table 3

SEQ ID	Database entry ID	Description	Results*
1247	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 1.643e-13 234-247 PR00048A 10.52 4.214e-13 318-331 PR00048A 10.52 4.857e-13 178-191 PR00048A 10.52 5.500e-13 402-415 PR00048A 10.52 1.000e-12 430-443 PR00048A 10.52 3.118e-12 262-275 PR00048A 10.52 4.176e-12 346-359 PR00048B 6.02 5.000e-12 222-231 PR00048B 6.02 5.000e-12 306-315 PR00048B 6.02 1.000e-11 390-399 PR00048B 6.02 2.385e-11 250-259 PR00048B 6.02 4.462e-11 166-175 PR00048A 10.52 5.263e-11 206-219 PR00048A 10.52 6.684e-11 290-303 PR00048A 10.52 7.632e-11 458-471 PR00048B 6.02 2.125e-10 362-371 PR00048A 10.52 5.304e-10 374-387 PR00048B 6.02 7.188e-10 194-203 PR00048B 6.02 1.474e-09 278-287 PR00048B 6.02 9.526e-09 446-455
1248	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 8.909e-33 183-228
1249	PD01876	ANTIGEN MELANOMA-ASSOCIATED MULTIGENE FAMILY TUM.	PD01876C 21.73 8.281e-15 66-118
1252	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 6.143e-10 304-318
1253	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 8.548e-10 1014-1026 PR00360B 13.61 3.045e-09 1052-1065
1253	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 9.464e-09 226-238
1254	PF00168	C2 domain proteins.	PF00168C 27.49 5.091e-10 1026-1051
1254	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 8.548e-10 1014-1026 PR00360B 13.61 3.045e-09 1043-1056
1254	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 9.464e-09 226-238
1255	PF00013	KH domain proteins family of RNA binding proteins.	PF00013 5.78 5.846e-11 57-68 PF00013 5.78 4.176e-10 378-389 PF00013 5.78 4.150e-09 135-146
1259	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 4.081e-10 1405-1458 BL01160B 19.54 8.784e-10 1268-1321 BL01160B 19.54 9.270e-10 69-122
1261	PR00401	SH2 DOMAIN SIGNATURE	PR00401A 14.00 3.348e-13 341-355
1261	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.697e-11 77-91
1261	PR00678	PI3 KINASE P85 REGULATORY	PR00678H 9.13 7.632e-09 347-

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Table 3

SEQ ID	Database entry ID	Description	Results*
		SUBUNIT SIGNATURE	369
1261	BL50001	Src homology 2 (SH2) domain proteins profile.	BL50001D 11.00 1.000e-08 337-347
1267	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 5.714e-10 180-188
1267	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 2.929e-10 137-151 PR00049D 0.00 1.153e-09 134-148 PR00049D 0.00 8.932e-09 136-150 PR00049D 0.00 9.390e-09 138-152
1269	PR00918	CALICIVIRUS NON-STRUCTURAL POLYPROTEIN FAMILY SIGNATURE	PR00918A 13.76 2.500e-11 1836-1856
1269	BL00674	AAA-protein family proteins.	BL00674B 4.46 9.614e-10 1839-1860
1269	BL00113	Adenylate kinase proteins.	BL00113A 12.74 1.415e-09 1843-1859
1269	BL00970	Nuclear transition protein 2 proteins.	BL00970B 10.09 3.176e-09 210-235
1269	BL00415	Synapsins proteins.	BL00415N 4.29 4.435e-10 1605-1648 BL00415N 4.29 7.307e-09 150-193
1269	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 9.928e-11 168-216 BL00115Z 3.12 9.721e-10 189-237 BL00115Z 3.12 6.824e-09 161-209 BL00115Z 3.12 8.743e-09 182-230
1269	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 9.167e-09 1615-1635
1269	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 2.214e-10 1548-1562 PR00049D 0.00 2.714e-10 1550-1564 PR00049D 0.00 2.714e-10 1551-1565 PR00049D 0.00 2.525e-09 100-114 PR00049D 0.00 3.288e-09 9-23 PR00049D 0.00 4.051e-09 10-24 PR00049D 0.00 4.661e-09 1545-1559 PR00049D 0.00 5.119e-09 1544-1558 PR00049D 0.00 5.729e-09 1546-1560 PR00049D 0.00 5.881e-09 98-112 PR00049D 0.00 8.322e-09 97-111 PR00049D 0.00 8.475e-09 1552-1566 PR00049D 0.00 8.780e-09 1553-1567 PR00049D 0.00 9.237e-09 1549-1563
1269	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 8.929e-14 1531-1563 DM00215 19.43 4.375e-12 1537-1569 DM00215 19.43 2.929e-10 1526-1558 DM00215 19.43 6.143e-10 522-554 DM00215 19.43 6.464e-10 1532-1564 DM00215 19.43 7.107e-10 1536-1568 DM00215 19.43 2.525e-09 581-613 DM00215 19.43 2.831e-09 165-197 DM00215 19.43 3.136e-09 1530-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			1562 DM00215 19.43 3.593e-09 609-641 DM00215 19.43 4.661e-09 1521-1553 DM00215 19.43 4.966e-09 595-627 DM00215 19.43 7.254e-09 625-657 DM00215 19.43 7.864e-09 78-110 DM00215 19.43 8.627e-09 596-628 DM00215 19.43 8.780e-09 539-571 DM00215 19.43 9.542e-09 538-570
1272	PF00789	Domain present in ubiquitin-regulatory proteins.	PF00789C 20.98 4.000e-09 506-530
1272	BL00504	Fumarate reductase / succinate dehydrogenase FAD-binding site proteins.	BL00504A 10.76 7.000e-09 36-57
1274	PF00992	Troponin.	PF00992A 16.67 3.842e-09 29-63
1277	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 8.615e-13 61-73
1277	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761E 14.32 5.168e-09 206-224
1277	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 5.680e-09 410-423
1277	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 6.192e-11 413-429 BL00028 16.07 7.943e-09 440-456
1278	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e-16 97-109 PD00066 13.92 3.571e-12 69-81 PD00066 13.92 3.077e-10 432-444
1278	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 1.947e-11 22-35 PR00048A 10.52 3.368e-11 469-482 PR00048A 10.52 5.696e-10 50-63 PR00048A 10.52 4.960e-09 78-91 PR00048A 10.52 6.040e-09 441-454
1278	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 3.250e-13 25-41 BL00028 16.07 4.600e-13 444-460 BL00028 16.07 1.000e-12 53-69 BL00028 16.07 8.826e-12 472-488 BL00028 16.07 1.000e-10 416-432 BL00028 16.07 4.343e-09 109-125 BL00028 16.07 5.114e-09 230-246 BL00028 16.07 6.143e-09 81-97
1282	PF00628	PHD-finger.	PF00628 15.84 9.036e-10 223-237
1285	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972A 11.93 2.703e-15 81-98 BL00972D 22.55 3.512e-12 284-308 BL00972C 16.48 7.120e-11 193-207 BL00972E 20.72 7.517e-10 310-331
1287	BL01032	Protein phosphatase 2C proteins.	BL01032G 8.33 9.859e-10 328-341 BL01032H 11.25 4.600e-09 376-388 BL01032C 6.14 6.368e-09 120-129
1288	BL01032	Protein phosphatase 2C proteins.	BL01032G 8.33 9.859e-10 243-256 BL01032H 11.25 4.600e-09

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Table 3

SEQ ID	Database entry ID	Description	Results*
			291-303
1292	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 2.286e-09 360-372 PR00910A 2.51 8.607e-09 354-366
1292	PR00522	CANNABINOID RECEPTOR TYPE 1 SIGNATURE	PR00522D 6.75 9.730e-09 184-203
1294	BL01313	Lipoate-protein ligase B proteins.	BL01313C 22.27 6.595e-30 151-187 BL01313B 28.18 5.576e-18 85-121
1295	BL00225	Crystallins beta and gamma 'Greek key' motif proteins.	BL00225B 18.06 7.000e-35 311-345 BL00225B 18.06 7.000e-32 223-257 BL00225A 13.82 7.000e-21 191-211 BL00225A 13.82 1.818e-09 277-297
1299	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.705e-12 72-126
1299	PF00023	Ank repeat proteins.	PF00023A 16.03 5.875e-10 72-87
1299	DM01664	kw.	DM01664C 17.05 5.194e-09 200-242
1301	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 8.763e-10 422-452
1311	BL01073	Ribosomal protein L24e proteins.	BL01073 24.30 1.000e-40 35-84
1312	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 3.089e-09 620-635
1315	BL00545	Aldose 1-epimerase proteins.	BL00545C 11.28 7.353e-17 169-181 BL00545A 10.20 2.071e-15 73-88 BL00545D 16.23 7.382e-13 303-320 BL00545B 13.10 3.942e-09 140-152
1317	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 2.602e-09 229-282
1318	BL00604	Synaptophysin / synaptoporin proteins.	BL00604F 5.96 1.426e-09 21-65
1318	PD02059	CORE POLYPROTEIN PROTEIN GAG CONTAINS: P.	PD02059B 24.48 1.000e-09 1151-1185 PD02059B 24.48 1.507e-09 1140-1174
1318	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE	PR00929B 4.38 2.607e-09 844-855
1318	BL00904	Protein prenyltransferases alpha subunit repeat proteins proteins.	BL00904A 8.30 5.500e-11 508-557 BL00904A 8.30 2.277e-09 1176-1225 BL00904A 8.30 8.021e-09 1169-1218
1318	BL00291	Prion protein.	BL00291A 4.49 8.448e-09 24-58
1318	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.289e-15 509-523 PR00049D 0.00 9.926e-13 713-727 PR00049D 0.00 3.950e-11 715-729 PR00049D 0.00 5.613e-11 1172-1186 PR00049D 0.00 6.445e-11 1141-1155 PR00049D 0.00 7.202e-11 508-522 PR00049D 0.00 9.546e-11 712-726 PR00049D 0.00 9.622e-11 507-521 PR00049D 0.00 9.924e-11 511-525 PR00049D 0.00 2.143e-10 1139-1153 PR00049D 0.00 2.786e-10 1179-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			1193 PR00049D 0.00 7.286e-10 714-728 PR00049D 0.00 7.857e-10 716-730 PR00049D 0.00 8.286e-10 710-724 PR00049D 0.00 8.571e-10 1366-1380 PR00049D 0.00 9.786e-10 711-725 PR00049D 0.00 1.000e-09 510-524 PR00049D 0.00 1.000e-09 1182-1196 PR00049D 0.00 1.458e-09 1169-1183 PR00049D 0.00 1.458e-09 1170-1184 PR00049D 0.00 2.220e-09 1145-1159 PR00049D 0.00 2.983e-09 1171-1185 PR00049D 0.00 3.136e-09 1180-1194 PR00049D 0.00 3.288e-09 1143-1157 PR00049D 0.00 4.203e-09 155-169 PR00049D 0.00 6.034e-09 1135-1149 PR00049D 0.00 6.186e-09 1183-1197 PR00049D 0.00 6.949e-09 512-526 PR00049D 0.00 8.627e-09 464-478
1318	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 4.548e-10 1176-1196 PR00211B 0.86 2.333e-09 1163-1183 PR00211B 0.86 8.750e-09 1174-1194
1318	BL00415	Synapsins proteins.	BL00415N 4.29 4.416e-09 1136-1179 BL00415N 4.29 8.818e-09 1125-1168
1318	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 6.333e-10 1135-1147 PR00910A 2.51 7.444e-10 1137-1149 PR00910A 2.51 5.071e-09 1141-1153 PR00910A 2.51 9.357e-09 1143-1155
1318	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 1.675e-15 1164-1196 DM00215 19.43 3.475e-15 1149-1181 DM00215 19.43 5.950e-15 1153-1185 DM00215 19.43 7.214e-14 1124-1156 DM00215 19.43 5.696e-13 1152-1184 DM00215 19.43 7.652e-13 1143-1175 DM00215 19.43 8.826e-13 1129-1161 DM00215 19.43 3.625e-12 1165-1197 DM00215 19.43 4.375e-12 1123-1155 DM00215 19.43 6.250e-12 1159-1191 DM00215 19.43 7.750e-12 1160-1192 DM00215 19.43 8.125e-12 1162-1194 DM00215 19.43 8.313e-12 1163-1195 DM00215 19.43 9.063e-12 1158-1190 DM00215 19.43 1.882e-11 1154-1186 DM00215 19.43 5.412e-11 1126-1158 DM00215 19.43 8.941e-11 1169-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			1201 DM00215 19.43 9.294e-11 1125-1157 DM00215 19.43 9.824e-11 1139-1171 DM00215 19.43 1.804e-10 1166-1198 DM00215 19.43 1.964e-10 1133- 1165 DM00215 19.43 5.018e-10 1173-1205 DM00215 19.43 5.179e-10 1138-1170 DM00215 19.43 6.304e-10 1131-1163 DM00215 19.43 9.357e-10 1148- 1180 DM00215 19.43 9.518e-10 1181-1213 DM00215 19.43 9.839e-10 1179-1211 DM00215 19.43 2.373e-09 1176-1208 DM00215 19.43 2.525e-09 1134- 1166 DM00215 19.43 3.288e-09 1168-1200 DM00215 19.43 3.441e-09 1144-1176 DM00215 19.43 4.051e-09 1142-1174 DM00215 19.43 6.339e-09 1172- 1204 DM00215 19.43 7.254e-09 1113-1145 DM00215 19.43 8.322e-09 1150-1182 DM00215 19.43 8.322e-09 1151-1183 DM00215 19.43 8.322e-09 1174- 1206 DM00215 19.43 9.390e-09 1161-1193 DM00215 19.43 9.542e-09 1128-1160 DM00215 19.43 9.542e-09 1349-1381
1319	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 8.313e-37 29-67
1319	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 6.294e-14 513- 529 BL00028 16.07 9.471e-14 401-417 BL00028 16.07 1.450e- 13 485-501 BL00028 16.07 5.950e-13 345-361 BL00028 16.07 6.850e-13 289-305 BL00028 16.07 2.957e-12 233- 249 BL00028 16.07 7.652e-12 373-389 BL00028 16.07 1.000e- 11 317-333 BL00028 16.07 3.769e-11 457-473 BL00028 16.07 5.500e-11 261-277 BL00028 16.07 9.654e-11 429- 445
1319	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.200e-14 417- 429 PD00066 13.92 6.400e-14 361-373 PD00066 13.92 8.800e- 14 501-513 PD00066 13.92 5.500e-13 473-485 PD00066 13.92 8.000e-13 445-457 PD00066 13.92 5.286e-12 249- 261 PD00066 13.92 5.714e-12 277-289 PD00066 13.92 7.429e- 12 305-317 PD00066 13.92 9.143e-12 389-401 PD00066

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Table 3

SEQ ID	Database entry ID	Description	Results*
			13.92 3.348e-11 221-233 PD00066 13.92 7.231e-10 333-345
1319	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.545e-15 314-327 PR00048A 10.52 1.750e-14 454-467 PR00048A 10.52 8.500e-14 510-523 PR00048A 10.52 2.286e-13 286-299 PR00048A 10.52 6.143e-13 370-383 PR00048A 10.52 4.176e-12 398-411 PR00048A 10.52 7.882e-12 342-355 PR00048A 10.52 1.474e-11 482-495 PR00048A 10.52 3.368e-11 258-271 PR00048A 10.52 4.789e-11 426-439 PR00048B 6.02 6.538e-11 414-423 PR00048A 10.52 7.632e-11 230-243 PR00048B 6.02 3.250e-10 470-479 PR00048B 6.02 4.938e-10 358-367 PR00048B 6.02 6.063e-10 498-507 PR00048B 6.02 7.188e-10 386-395 PR00048B 6.02 9.053e-09 218-227
1324	BL00361	Ribosomal protein S10 proteins.	BL00361A 11.94 8.159e-11 52-67
1324	PR00971	RIBOSOMAL PROTEIN S10 FAMILY SIGNATURE	PR00971A 13.33 2.432e-09 19-32
1325	BL00027	'Homeobox' domain proteins.	BL00027 26.43 1.321e-17 822-864 BL00027 26.43 3.893e-17 1030-1072 BL00027 26.43 4.214e-17 560-602
1325	PR00028	POU DOMAIN SIGNATURE	PR00028E 15.68 3.700e-10 841-856
1325	BL00035	'POU' domain proteins.	BL00035C 17.40 6.092e-11 829-858 BL00035C 17.40 5.500e-10 1037-1066
1325	BL00032	'Homeobox' antennapedia-type protein.	BL00032C 11.28 5.743e-10 1058-1075
1325	PR00031	LAMBDA AND OTHER REPRESSOR HELIX-TURN-HELIX SIGNATURE	PR00031B 16.29 3.483e-10 845-861 PR00031B 16.29 6.586e-10 1053-1069
1325	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 2.080e-09 140-153
1325	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 3.898e-09 931-963
1325	PR00671	INHIBIN BETA B CHAIN SIGNATURE	PR00671C 4.18 5.966e-09 417-436
1325	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 6.034e-09 408-422
1325	BL00422	Granins proteins.	BL00422C 16.18 6.647e-09 649-676
1325	PF01140	Matrix protein (MA), p15.	PF01140D 15.54 6.965e-09 641-675
1325	PR00024	HOMEBOX SIGNATURE	PR00024C 7.49 3.077e-10 1062-1071 PR00024C 7.49 7.300e-09

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Table 3

SEQ ID	Database entry ID	Description	Results*
			592-601
1325	BL00870	Chaperonins clpA/B proteins.	BL00870F 8.73 7.417e-09 1058-1106
1325	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.771e-09 721-737 BL00028 16.07 7.686e-09 622-638
1327	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 9.250e-13 62-74
1327	PF00023	Ank repeat proteins.	PF00023B 14.20 1.500e-10 65-74
1327	PR00058	RIBOSOMAL PROTEIN L5 SIGNATURE	PR00058F 8.67 7.667e-09 230-250
1327	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 6.119e-09 36-90 PF00791B 28.49 8.596e-09 69-123
1330	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e-16 421-433 PD00066 13.92 4.462e-15 337-349 PD00066 13.92 4.462e-15 505-517 PD00066 13.92 1.600e-14 477-489 PD00066 13.92 2.200e-14 533-545 PD00066 13.92 2.800e-14 309-321 PD00066 13.92 7.000e-14 281-293 PD00066 13.92 7.000e-14 449-461 PD00066 13.92 2.500e-13 561-573 PD00066 13.92 8.286e-12 393-405 PD00066 13.92 2.174e-11 365-377
1330	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 8.941e-14 461-477 BL00028 16.07 6.850e-13 433-449 BL00028 16.07 7.300e-13 349-365 BL00028 16.07 2.174e-12 517-533 BL00028 16.07 6.087e-12 405-421 BL00028 16.07 8.043e-12 377-393 BL00028 16.07 3.077e-11 489-505 BL00028 16.07 3.423e-11 293-309 BL00028 16.07 7.231e-11 265-281 BL00028 16.07 7.231e-11 545-561 BL00028 16.07 7.923e-11 629-645 BL00028 16.07 6.100e-10 573-589
1330	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 9.727e-36 10-48 PD01066 19.43 3.743e-09 51-89
1330	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 1.000e-14 458-471 PR00048A 10.52 1.750e-14 514-527 PR00048A 10.52 4.750e-14 486-499 PR00048A 10.52 7.750e-14 402-415 PR00048A 10.52 7.429e-13 346-359 PR00048A 10.52 8.714e-13 542-555 PR00048A 10.52 2.588e-12 430-443 PR00048A 10.52 2.421e-11 570-583 PR00048B 6.02 1.563e-10 306-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			315 PR00048B 6.02 2.688e-10 418-427 PR00048A 10.52 3.348e-10 290-303 PR00048B 6.02 4.375e-10 446-455 PR00048B 6.02 5.500e-10 278- 287 PR00048B 6.02 5.500e-10 502-511 PR00048B 6.02 3.842e- 09 474-483 PR00048B 6.02 5.263e-09 334-343 PR00048A 10.52 6.400e-09 374-387 PR00048B 6.02 7.632e-09 530- 539 PR00048B 6.02 7.632e-09 558-567
1331	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 7.210e-10 214- 252
1332	PR00403	WW DOMAIN SIGNATURE	PR00403B 12.19 9.600e-12 81-95
1332	PF00620	GTPase-activator protein for Rho-like GTPases.	PF00620B 14.20 6.250e-10 966- 982
1332	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 1.655e-09 81-95
1332	PD01351	PROTEIN REPEAT NEUROFILAMENT TRIPL.	PD01351B 13.72 5.500e-09 131- 156
1333	DM01774	INSECT IRIDESCENT VIRUS REPETITIVE PROTEIN.	DM01774 10.00 7.429e-09 36-78
1333	PR00500	POLYCYSTIC KIDNEY DISEASE PROTEIN SIGNATURE	PR00500B 7.74 8.389e-09 148- 168
1334	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE	PR00300A 9.56 3.662e-10 1025- 1043
1334	PR00830	ENDOPEPTIDASE LA (LON) SERINE PROTEASE (S16) SIGNATURE	PR00830A 8.41 4.441e-10 1029- 1048
1334	BL00662	Bacterial type II secretion system protein E proteins.	BL00662D 8.67 7.035e-10 1021- 1041
1334	BL00674	AAA-protein family proteins.	BL00674B 4.46 8.200e-10 1022- 1043
1334	BL01008	DnaA protein.	BL01008B 12.53 8.780e-10 1022- 1036
1334	BL01128	Shikimate kinase proteins.	BL01128A 18.84 4.977e-09 1025- 1058
1334	PR00051	BACTERIAL CHROMOSOMAL REPLICATION INITIATOR (DNAA) SIGNATURE	PR00051A 10.68 9.292e-09 1022- 1042
1337	PR00625	DNAJ PROTEIN FAMILY SIGNATURE	PR00625B 13.48 2.853e-10 59-79 PR00625A 12.84 5.299e-10 22-41
1337	BL00636	Nt-dnaJ domain proteins.	BL00636B 15.11 5.500e-10 59-79 BL00636A 8.07 9.571e-10 26-42
1344	PD00066	PROTEIN ZINC-FINGER METAL- BINDI.	PD00066 13.92 8.200e-17 162- 174 PD00066 13.92 5.846e-15 330-342 PD00066 13.92 3.500e- 13 190-202 PD00066 13.92 9.000e-13 218-230 PD00066 13.92 1.429e-12 358-370 PD00066 13.92 2.714e-12 302- 314 PD00066 13.92 8.286e-12 274-286 PD00066 13.92 2.174e- 11 246-258
1344	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 6.294e-14 342-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			358 BL00028 16.07 4.522e-12 258-274 BL00028 16.07 9.609e-12 314-330 BL00028 16.07 1.346e-11 286-302 BL00028 16.07 2.385e-11 174-190 BL00028 16.07 3.769e-11 146-162 BL00028 16.07 6.192e-11 370-386 BL00028 16.07 9.654e-11 230-246 BL00028 16.07 5.800e-10 202-218
1344	BL01030	RNA polymerases M / 15 Kd subunits proteins.	BL01030 23.44 5.557e-09 230-267
1344	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 1.643e-13 311-324 PR00048A 10.52 7.429e-13 283-296 PR00048A 10.52 2.588e-12 171-184 PR00048A 10.52 7.882e-12 255-268 PR00048A 10.52 8.412e-12 339-352 PR00048A 10.52 1.474e-11 143-156 PR00048B 6.02 5.846e-11 215-224 PR00048A 10.52 7.158e-11 227-240 PR00048B 6.02 8.615e-11 355-364 PR00048A 10.52 1.783e-10 199-212 PR00048A 10.52 2.174e-10 367-380 PR00048B 6.02 4.375e-10 327-336 PR00048B 6.02 4.938e-10 159-168 PR00048B 6.02 7.158e-09 187-196 PR00048B 6.02 9.526e-09 271-280
1349	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 1.750e-28 50-88
1349	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e-16 297-309 PD00066 13.92 8.200e-16 353-365 PD00066 13.92 7.000e-13 269-281 PD00066 13.92 9.217e-11 325-337 PD00066 13.92 9.217e-11 381-393 PD00066 13.92 9.217e-11 409-421
1349	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 8.200e-13 365-381 BL00028 16.07 1.000e-12 253-269 BL00028 16.07 2.957e-12 393-409 BL00028 16.07 3.739e-12 309-325 BL00028 16.07 1.900e-10 281-297 BL00028 16.07 3.400e-10 337-353 BL00028 16.07 5.500e-10 421-437
1349	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 5.091e-15 306-319 PR00048A 10.52 6.250e-14 362-375 PR00048A 10.52 1.000e-13 390-403 PR00048B 6.02 5.000e-12 294-303 PR00048B 6.02 5.000e-12 350-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			359 PR00048A 10.52 6.294e-12 418-431 PR00048A 10.52 7.158e-11 334-347 PR00048A 10.52 8.826e-10 250-263 PR00048A 10.52 8.826e-10 278- 291 PR00048B 6.02 6.211e-09 266-275 PR00048B 6.02 9.526e- 09 434-443
1351	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479A 19.86 3.000e-11 103- 125 BL00479B 12.57 3.340e-10 129-144
1351	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002B 15.18 5.000e-09 327- 340
1351	PR00452	SH3 DOMAIN SIGNATURE	PR00452D 17.02 6.192e-09 329- 341
1352	BL00113	Adenylate kinase proteins.	BL00113A 12.74 6.571e-17 297- 313 BL00113A 12.74 5.154e-14 53-69
1352	PR00094	ADENYLATE KINASE SIGNATURE	PR00094A 10.31 6.760e-15 297- 310 PR00094A 10.31 1.000e-13 53-66 PR00094C 12.94 7.789e-10 132-148
1352	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 8.809e-10 293- 310
1352	BL01128	Shikimate kinase proteins.	BL01128A 18.84 5.814e-09 296- 329
1356	BL01077	Ribosomal protein L37e proteins.	BL01077 16.34 1.000e-40 3-49
1358	PF00992	Troponin.	PF00992A 16.67 2.161e-25 168- 202 PF00992B 26.31 7.818e-23 246-280 PF00992C 16.35 9.743e- 15 309-326
1358	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301B 5.49 5.091e-10 193- 203
1359	DM00475	w LOW TRANSPOSASE SAPA 12K.	DM00475B 12.12 4.462e-09 103- 122
1359	BL00226	Intermediate filaments proteins.	BL00226B 23.86 6.233e-09 197- 244
1360	PF00852	Fucosyl transferase.	PF00852F 15.97 7.889e-18 328- 364
1361	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 5.286e-10 243- 251
1361	BL01282	BIR repeat proteins.	BL01282B 30.49 9.455e-10 224- 262
1362	PF00075	RNase H.	PF00075B 12.56 6.276e-12 274- 284 PF00075A 14.44 8.560e-12 227-243 PF00075F 12.87 4.750e- 11 704-714 PF00075C 11.58 9.786e-11 306-317
1362	BL00349	CTF/NF-I proteins.	BL00349C 9.33 1.000e-09 738- 780
1364	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 8.636e-36 29-67
1367	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 4.000e-28 36-74
1367	PD00066	PROTEIN ZINC-FINGER METAL-	PD00066 13.92 9.100e-16 786-

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Table 3

SEQ ID	Database entry ID	Description	Results*
		BINDI.	798 PD00066 13.92 3.077e-15 423-435 PD00066 13.92 3.077e-15 702-714 PD00066 13.92 4.462e-15 395-407 PD00066 13.92 4.462e-15 562-574 PD00066 13.92 4.462e-15 618-630 PD00066 13.92 4.462e-15 758-770 PD00066 13.92 7.231e-15 535-547 PD00066 13.92 1.600e-14 479-491 PD00066 13.92 1.600e-14 646-658 PD00066 13.92 6.400e-14 674-686 PD00066 13.92 7.000e-14 730-742 PD00066 13.92 3.500e-13 590-602 PD00066 13.92 2.286e-12 451-463 PD00066 13.92 4.808e-10 367-379
1367	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.350e-13 379-395 BL00028 16.07 3.348e-12 435-451 BL00028 16.07 9.217e-12 463-479 BL00028 16.07 9.217e-12 574-590 BL00028 16.07 1.692e-11 742-758 BL00028 16.07 2.038e-11 686-702 BL00028 16.07 2.731e-11 491-507 BL00028 16.07 6.885e-11 658-674 BL00028 16.07 6.885e-11 770-786 BL00028 16.07 7.577e-11 407-423 BL00028 16.07 7.577e-11 630-646 BL00028 16.07 8.269e-11 519-535 BL00028 16.07 1.300e-10 602-618 BL00028 16.07 5.200e-10 351-367 BL00028 16.07 1.514e-09 798-814 BL00028 16.07 6.657e-09 714-730
1367	BL00152	ATP synthase alpha and beta subunits proteins.	BL00152F 12.70 8.650e-09 49-58
1367	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 4.750e-14 376-389 PR00048A 10.52 1.000e-13 404-417 PR00048A 10.52 1.000e-13 571-584 PR00048A 10.52 4.214e-13 627-640 PR00048A 10.52 8.071e-13 460-473 PR00048A 10.52 1.000e-12 767-780 PR00048A 10.52 3.118e-12 488-501 PR00048A 10.52 7.353e-12 432-445 PR00048A 10.52 4.316e-11 739-752 PR00048A 10.52 4.789e-11 655-668 PR00048A 10.52 9.053e-11 599-612 PR00048B 6.02 9.308e-11 671-680 PR00048A 10.52 9.526e-11 683-696 PR00048A 10.52 2.565e-10

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Table 3

SEQ ID	Database entry ID	Description	Results*
			348-361 PR00048A 10.52 5.304e-10 795-808 PR00048B 6.02 6.063e-10 755-764 PR00048B 6.02 8.313e-10 699- 708 PR00048B 6.02 8.313e-10 783-792 PR00048A 10.52 8.435e-10 711-724 PR00048B 6.02 9.438e-10 587-596 PR00048B 6.02 1.474e-09 476- 485 PR00048B 6.02 2.895e-09 559-568 PR00048B 6.02 3.368e- 09 420-429 PR00048B 6.02 5.737e-09 392-401 PR00048B 6.02 9.053e-09 615-624 PR00048B 6.02 9.053e-09 643- 652 PR00048A 10.52 9.280e-09 516-529 PR00048B 6.02 1.000e- 08 504-513
1369	BL00674	AAA-protein family proteins.	BL00674B 4.46 1.730e-09 71-92
1369	DM00315	072 RIBONUCLEASE INHIBITOR.	DM00315G 15.85 5.562e-16 709- 744 DM00315G 15.85 8.700e-11 766-801 DM00315D 18.40 1.535e-10 710-753 DM00315G 15.85 7.128e-10 652-687 DM00315G 15.85 5.770e-09 595- 630
1369	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.333e-09 690- 703 PR00019A 11.19 7.333e-09 747-760
1370	BL00633	Bromodomain proteins.	BL00633B 13.82 6.657e-15 136- 160
1370	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.786e-10 907- 921
1370	PR00503	BROMODOMAIN SIGNATURE	PR00503B 9.96 6.786e-13 135- 151 PR00503D 20.81 2.023e-12 169-188 PR00503C 19.84 2.688e- 09 151-169
1370	BL00224	Clathrin light chain proteins.	BL00224B 16.94 3.618e-09 11-63
1371	PR00756	MEMBRANE ALANYL DIPEPTIDASE (M1) FAMILY SIGNATURE	PR00756D 10.58 4.484e-17 330- 345 PR00756E 11.91 4.094e-13 349-361 PR00756A 12.90 3.571e-12 184-199 PR00756C 11.60 7.900e-12 303-313 PR00756B 14.06 2.653e-10 228- 243
1371	BL00142	Neutral zinc metallopeptidases, zinc- binding region proteins.	BL00142 8.38 5.286e-09 330-340
1372	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 3.368e-09 393- 402
1372	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PD02784B 26.46 5.245e-09 389- 431
1372	PF00761	Polyomavirus coat protein.	PF00761B 18.21 8.633e-09 227- 265
1376	PD00066	PROTEIN ZINC-FINGER METAL- BINDI.	PD00066 13.92 7.300e-17 212- 224 PD00066 13.92 7.300e-17

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Table 3

SEQ ID	Database entry ID	Description	Results*
			464-476 PD00066 13.92 8.200e-16 268-280 PD00066 13.92 9.308e-15 296-308 PD00066 13.92 2.800e-14 156-168 PD00066 13.92 2.800e-14 184-196 PD00066 13.92 2.800e-14 436-448 PD00066 13.92 5.200e-14 380-392 PD00066 13.92 5.800e-14 240-252 PD00066 13.92 3.000e-13 324-336 PD00066 13.92 3.000e-13 408-420 PD00066 13.92 6.087e-11 352-364
1376	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970A 8.50 1.000e-09 391-397
1376	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.929e-16 476-492 BL00028 16.07 5.050e-13 196-212 BL00028 16.07 5.950e-13 280-296 BL00028 16.07 6.850e-13 420-436 BL00028 16.07 8.650e-13 252-268 BL00028 16.07 8.043e-12 224-240 BL00028 16.07 8.826e-12 364-380 BL00028 16.07 1.346e-11 336-352 BL00028 16.07 3.423e-11 308-324 BL00028 16.07 6.538e-11 140-156 BL00028 16.07 3.400e-10 448-464 BL00028 16.07 8.500e-10 168-184 BL00028 16.07 2.543e-09 392-408
1376	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 5.500e-17 473-486 PR00048A 10.52 8.500e-17 193-206 PR00048A 10.52 1.000e-16 277-290 PR00048A 10.52 1.000e-16 417-430 PR00048A 10.52 2.636e-15 249-262 PR00048A 10.52 4.000e-14 333-346 PR00048A 10.52 2.929e-13 305-318 PR00048A 10.52 4.214e-13 361-374 PR00048A 10.52 1.529e-12 221-234 PR00048B 6.02 1.000e-11 209-218 PR00048B 6.02 1.000e-11 265-274 PR00048B 6.02 1.000e-11 461-470 PR00048A 10.52 2.895e-11 445-458 PR00048B 6.02 4.462e-11 181-190 PR00048A 10.52 7.158e-11 165-178 PR00048B 6.02 7.231e-11 377-386 PR00048B 6.02 2.688e-10 433-442 PR00048B 6.02 3.250e-10 153-162 PR00048B 6.02 7.750e-10 293-302 PR00048B 6.02 8.875e-10 237-246 PR00048B 6.02 3.842e-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			09 321-330 PR00048B 6.02 3.842e-09 405-414 PR00048A 10.52 8.560e-09 137-150 PR00048A 10.52 9.280e-09 389- 402
1377	PD02448	TRANSCRIPTION PROTEIN DNA-BINDIN.	PD02448A 9.37 4.000e-09 47-85
1377	BL00353	HMG1/2 proteins.	BL00353B 11.47 7.236e-09 25-74
1379	BL00926	Lysyl oxidase copper-binding region proteins.	BL00926B 13.84 6.580e-10 668-705
1379	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 9.801e-09 648-696
1380	BL01240	Purine and other phosphorylases family 2 proteins.	BL01240C 25.01 5.645e-33 177-218 BL01240B 22.37 9.550e-26 96-126 BL01240A 11.26 1.243e-11 10-23
1386	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 8.800e-10 638-654 BL00028 16.07 5.371e-09 214-230 BL00028 16.07 1.000e-08 791-807
1389	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.500e-15 206-222 BL00028 16.07 6.063e-15 178-194 BL00028 16.07 7.188e-15 290-306 BL00028 16.07 1.000e-14 150-166 BL00028 16.07 2.800e-13 122-138 BL00028 16.07 4.600e-13 458-474 BL00028 16.07 1.000e-12 430-446 BL00028 16.07 3.348e-12 534-550 BL00028 16.07 5.696e-12 234-250 BL00028 16.07 6.478e-12 318-334 BL00028 16.07 4.462e-11 402-418 BL00028 16.07 5.154e-11 374-390 BL00028 16.07 6.192e-11 262-278 BL00028 16.07 8.615e-11 94-110 BL00028 16.07 4.600e-10 346-362
1389	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e-14 250-262 PD00066 13.92 2.500e-13 222-234 PD00066 13.92 2.500e-13 390-402 PD00066 13.92 7.500e-13 306-318 PD00066 13.92 5.286e-12 194-206 PD00066 13.92 8.286e-12 110-122 PD00066 13.92 8.714e-12 334-346 PD00066 13.92 1.000e-11 138-150 PD00066 13.92 1.000e-11 418-430 PD00066 13.92 1.000e-11 446-458 PD00066 13.92 7.261e-11 362-374 PD00066 13.92 9.609e-11 278-290 PD00066 13.92 1.692e-10 474-486 PD00066 13.92 2.200e-09 494-506
1389	BL00479	Phorbol esters / diacylglycerol binding	BL00479A 19.86 9.234e-09 81-

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Table 3

SEQ ID	Database entry ID	Description	Results*
		domain proteins.	103
1389	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 3.250e-16 203-216 PR00048A 10.52 5.091e-15 287-300 PR00048A 10.52 6.727e-15 147-160 PR00048A 10.52 6.727e-15 455-468 PR00048A 10.52 1.000e-14 427-440 PR00048A 10.52 2.500e-14 119-132 PR00048A 10.52 4.000e-14 315-328 PR00048A 10.52 4.857e-13 531-544 PR00048A 10.52 2.059e-12 399-412 PR00048A 10.52 3.118e-12 343-356 PR00048A 10.52 3.118e-12 371-384 PR00048A 10.52 4.706e-12 259-272 PR00048A 10.52 5.235e-12 231-244 PR00048A 10.52 8.941e-12 91-104 PR00048B 6.02 1.000e-10 247-256 PR00048A 10.52 4.913e-10 175-188 PR00048B 6.02 2.421e-09 471-480 PR00048B 6.02 3.842e-09 163-172 PR00048A 10.52 4.240e-09 503-516 PR00048B 6.02 7.632e-09 219-228 PR00048B 6.02 9.526e-09 191-200
1391	BL00411	Kinesin motor domain proteins.	BL00411G 21.39 2.667e-30 136-177 BL00411E 10.43 9.419e-16 31-49 BL00411F 14.77 1.529e-14 92-116 BL00411H 15.66 6.684e-14 185-215
1391	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380B 12.64 6.362e-13 101-118 PR00380C 13.18 1.783e-12 135-153 PR00380D 9.93 3.803e-12 186-207
1395	BL01283	T-box domain proteins.	BL01283A 24.15 6.906e-39 122-169 BL01283D 11.70 7.868e-31 272-304 BL01283B 23.17 9.757e-31 182-223 BL01283C 13.05 8.448e-16 234-247
1395	PR00937	T-BOX DOMAIN SIGNATURE	PR00937A 15.25 1.000e-25 130-154 PR00937D 13.41 7.375e-17 233-247 PR00937E 11.86 8.541e-14 275-288 PR00937F 12.53 1.450e-12 296-304 PR00937C 10.51 3.400e-12 214-223 PR00937B 14.58 1.628e-11 197-210
1397	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.000e-15 339-355 BL00028 16.07 1.000e-14 535-551 BL00028 16.07 2.800e-13 479-495 BL00028 16.07 5.500e-13 199-215 BL00028 16.07 7.750e-13 283-299 BL00028 16.07 8.200e-13 255-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			271 BL00028 16.07 4.913e-12 395-411 BL00028 16.07 6.478e-12 423-439 BL00028 16.07 3.077e-11 311-327 BL00028 16.07 3.077e-11 507-523 BL00028 16.07 4.462e-11 451-467 BL00028 16.07 8.615e-11 227-243 BL00028 16.07 5.200e-10 563-579 BL00028 16.07 7.000e-10 367-383
1397	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.800e-14 271-283 PD00066 13.92 8.800e-14 467-479 PD00066 13.92 2.000e-13 523-535 PD00066 13.92 2.500e-13 411-423 PD00066 13.92 5.000e-13 215-227 PD00066 13.92 5.500e-13 495-507 PD00066 13.92 2.286e-12 551-563 PD00066 13.92 7.000e-12 327-339 PD00066 13.92 1.346e-10 243-255 PD00066 13.92 2.385e-10 299-311 PD00066 13.92 8.269e-10 439-451 PD00066 13.92 8.200e-09 383-395
1397	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 6.625e-16 532-545 PR00048A 10.52 4.273e-15 280-293 PR00048A 10.52 6.250e-14 336-349 PR00048A 10.52 6.250e-14 420-433 PR00048A 10.52 7.000e-14 476-489 PR00048A 10.52 8.500e-14 308-321 PR00048A 10.52 4.214e-13 448-461 PR00048A 10.52 1.000e-11 252-265 PR00048A 10.52 3.368e-11 196-209 PR00048A 10.52 3.368e-11 224-237 PR00048A 10.52 4.316e-11 392-405 PR00048A 10.52 4.789e-11 364-377 PR00048B 6.02 7.923e-11 296-305 PR00048B 6.02 2.688e-10 492-501 PR00048B 6.02 3.813e-10 324-333 PR00048B 6.02 4.375e-10 240-249 PR00048A 10.52 4.913e-10 560-573 PR00048B 6.02 8.875e-10 520-529 PR00048A 10.52 9.609e-10 504-517 PR00048B 6.02 3.368e-09 464-473 PR00048B 6.02 5.263e-09 548-557 PR00048B 6.02 6.211e-09 408-417 PR00048B 6.02 9.053e-09 268-277
1398	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 6.824e-10 211-225 PR00320C 13.01 8.800e-09

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Table 3

SEQ ID	Database entry ID	Description	Results*
			211-225
1401	BL00359	Ribosomal protein L11 proteins.	BL00359B 23.07 4.231e-24 46-86 BL00359C 22.18 6.586e-22 101-134 BL00359A 20.66 8.297e-13 10-45
1401	BL01108	Ribosomal protein L24 proteins.	BL01108A 20.33 1.000e-08 30-62
1403	PF00855	PWWP domain proteins.	PF00855 13.75 8.116e-18 357-373
1404	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 3.118e-14 576-592 BL00028 16.07 4.706e-14 436-452 BL00028 16.07 5.765e-14 772-788 BL00028 16.07 7.882e-14 212-228 BL00028 16.07 3.700e-13 632-648 BL00028 16.07 6.400e-13 296-312 BL00028 16.07 8.650e-13 240-256 BL00028 16.07 9.100e-13 856-872 BL00028 16.07 9.550e-13 688-704 BL00028 16.07 1.000e-12 268-284 BL00028 16.07 5.304e-12 660-676 BL00028 16.07 6.087e-12 604-620 BL00028 16.07 6.478e-12 520-536 BL00028 16.07 8.435e-12 156-172 BL00028 16.07 8.826e-12 716-732 BL00028 16.07 1.000e-11 324-340 BL00028 16.07 1.000e-11 380-396 BL00028 16.07 2.038e-11 548-564 BL00028 16.07 2.038e-11 744-760 BL00028 16.07 2.385e-11 800-816 BL00028 16.07 5.500e-11 184-200 BL00028 16.07 5.500e-11 352-368 BL00028 16.07 5.500e-11 408-424 BL00028 16.07 7.231e-11 828-844 BL00028 16.07 1.900e-10 464-480
1404	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 1.000e-14 256-268 PD00066 13.92 1.000e-14 312-324 PD00066 13.92 1.000e-14 340-352 PD00066 13.92 1.000e-14 396-408 PD00066 13.92 1.000e-14 592-604 PD00066 13.92 4.600e-14 648-660 PD00066 13.92 5.200e-14 368-380 PD00066 13.92 5.200e-14 676-688 PD00066 13.92 8.800e-14 284-296 PD00066 13.92 1.500e-13 564-576 PD00066 13.92 2.000e-13 788-800 PD00066 13.92 5.500e-13 816-828 PD00066 13.92 6.000e-13 452-464 PD00066 13.92 1.000e-12 704-716 PD00066 13.92 1.429e-12 620-632 PD00066 13.92 1.429e-12 760-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			772 PD00066 13.92 4.000e-12 844-856 PD00066 13.92 6.571e-12 536-548 PD00066 13.92 6.571e-12 732-744 PD00066 13.92 1.000e-11 172-184 PD00066 13.92 4.462e-10 228-240 PD00066 13.92 8.200e-09 200-212
1404	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479A 19.86 8.660e-09 507-529
1404	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.500e-17 629-642 PR00048A 10.52 2.500e-14 657-670 PR00048A 10.52 4.000e-14 573-586 PR00048A 10.52 9.250e-14 769-782 PR00048A 10.52 1.000e-13 853-866 PR00048A 10.52 5.500e-13 265-278 PR00048A 10.52 8.714e-13 741-754 PR00048A 10.52 8.714e-13 825-838 PR00048A 10.52 9.357e-13 293-306 PR00048A 10.52 1.000e-12 377-390 PR00048A 10.52 3.118e-12 209-222 PR00048A 10.52 3.118e-12 713-726 PR00048A 10.52 4.706e-12 601-614 PR00048B 6.02 1.000e-11 561-570 PR00048A 10.52 2.421e-11 237-250 PR00048A 10.52 2.421e-11 797-810 PR00048A 10.52 4.789e-11 181-194 PR00048A 10.52 5.263e-11 321-334 PR00048B 6.02 5.846e-11 365-374 PR00048A 10.52 7.632e-11 349-362 PR00048A 10.52 7.632e-11 405-418 PR00048A 10.52 7.632e-11 545-558 PR00048B 6.02 8.615e-11 673-682 PR00048A 10.52 9.053e-11 461-474 PR00048A 10.52 2.174e-10 685-698 PR00048B 6.02 4.375e-10 869-878 PR00048A 10.52 4.913e-10 153-166 PR00048B 6.02 5.500e-10 281-290 PR00048B 6.02 5.500e-10 309-318 PR00048B 6.02 5.737e-09 701-710 PR00048B 6.02 5.737e-09 813-822 PR00048A 10.52 6.040e-09 433-446 PR00048B 6.02 6.684e-09 589-598 PR00048B 6.02 7.632e-09 421-430 PR00048B 6.02 8.579e-09 533-542 PR00048B 6.02 9.053e-09 645-654 PR00048B 6.02 9.053e-09 785-794

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Table 3

SEQ ID	Database entry ID	Description	Results*
1404	PD02462	PROTEIN BOLA TRANSCRIPTION REGULATION AC.	PD02462A 22.48 8.177e-10 345-379 PD02462A 22.48 4.841e-09 541-575 PD02462A 22.48 5.720e-09 261-295 PD02462A 22.48 8.244e-09 653-687 PD02462A 22.48 9.451e-09 401-435
1408	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.716e-13 290-302 DM01970B 8.60 2.157e-12 173-185
1408	BL00609	Glycosyl hydrolases family 32 proteins.	BL00609D 14.32 9.082e-09 63-74
1413	PR00598	BACTERIAL REGULATORY PROTEIN MARR FAMILY SIGNATURE	PR00598D 16.48 6.434e-09 153-173
1415	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 3.593e-15 62-74
1415	PR00802	SERUM ALBUMIN FAMILY SIGNATURE	PR00802A 12.17 3.213e-09 76-90
1417	BL00019	Actinin-type actin-binding domain proteins.	BL00019D 15.33 3.769e-16 984-1013
1420	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 3.077e-12 433-448 BL00107A 18.39 8.615e-12 371-401
1420	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109D 17.04 6.492e-10 434-456
1425	BL00194	Thioredoxin family proteins.	BL00194 12.16 7.667e-12 31-43
1425	PR00421	THIOREDOXIN FAMILY SIGNATURE	PR00421B 11.40 6.800e-09 38-47
1427	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 6.447e-09 78-97
1430	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 7.955e-14 83-137 PF00791B 28.49 5.091e-11 149-203 PF00791B 28.49 6.854e-10 182-236 PF00791B 28.49 7.029e-10 116-170 PF00791B 28.49 8.252e-10 50-104
1430	PF00023	Ank repeat proteins.	PF00023A 16.03 6.625e-10 50-65 PF00023A 16.03 4.857e-09 149-164 PF00023A 16.03 7.107e-09 83-98
1431	PR00547	X OPIOID RECEPTOR SIGNATURE	PR00547G 14.01 7.261e-09 91-108
1431	BL00038	Myc-type, 'helix-loop-helix' dimerization domain proteins.	BL00038A 13.61 7.300e-09 121-136
1431	BL00873	Sodium:alanine symporter family proteins.	BL00873C 13.14 8.962e-09 49-80
1431	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 3.232e-11 199-247 BL00115Z 3.12 1.000e-09 192-240 BL00115Z 3.12 9.338e-09 206-254
1434	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.000e-14 782-798 BL00028 16.07 4.706e-14 698-714 BL00028 16.07 7.882e-14 502-518 BL00028 16.07 5.500e-13 614-630 BL00028 16.07 5.950e-13 558-574 BL00028 16.07 2.174e-12 362-378 BL00028 16.07 2.174e-12 922-938 BL00028 16.07 2.565e-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			12 306-322 BL00028 16.07 2.957e-12 754-770 BL00028 16.07 5.696e-12 418-434 BL00028 16.07 8.043e-12 894- 910 BL00028 16.07 9.217e-12 866-882 BL00028 16.07 2.038e- 11 642-658 BL00028 16.07 3.769e-11 446-462 BL00028 16.07 4.115e-11 810-826 BL00028 16.07 6.538e-11 278- 294 BL00028 16.07 8.615e-11 726-742 BL00028 16.07 8.962e- 11 530-546 BL00028 16.07 1.300e-10 390-406 BL00028 16.07 2.200e-10 334-350 BL00028 16.07 5.200e-10 586- 602 BL00028 16.07 9.100e-10 474-490 BL00028 16.07 9.100e- 10 670-686
1434	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 9.100e-17 630- 642 PD00066 13.92 1.000e-15 798-810 PD00066 13.92 4.462e- 15 434-446 PD00066 13.92 5.846e-15 882-894 PD00066 13.92 1.600e-14 714-726 PD00066 13.92 4.000e-14 770- 782 PD00066 13.92 5.800e-14 406-418 PD00066 13.92 5.800e- 14 574-586 PD00066 13.92 6.400e-14 602-614 PD00066 13.92 7.500e-13 378-390 PD00066 13.92 9.000e-13 686- 698 PD00066 13.92 3.143e-12 294-306 PD00066 13.92 4.522e- 11 490-502 PD00066 13.92 4.913e-11 854-866 PD00066 13.92 8.435e-11 350-362 PD00066 13.92 8.435e-11 546- 558 PD00066 13.92 8.435e-11 742-754 PD00066 13.92 2.385e- 10 658-670 PD00066 13.92 2.385e-10 910-922 PD00066 13.92 3.077e-10 462-474 PD00066 13.92 5.500e-09 826- 838
1434	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 3.930e-31 83-121 PD01066 19.43 9.143e-09 124- 162
1434	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 1.000e-17 555- 568 PR00048A 10.52 1.000e-14 751-764 PR00048A 10.52 5.500e-14 863-876 PR00048A 10.52 9.250e-14 919-932 PR00048A 10.52 1.000e-13 891- 904 PR00048A 10.52 2.929e-13 807-820 PR00048A 10.52

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Table 3

SEQ ID	Database entry ID	Description	Results*
			3.571e-13 359-372 PR00048A 10.52 3.571e-13 779-792 PR00048A 10.52 4.214e-13 499-512 PR00048A 10.52 3.118e-12 415-428 PR00048A 10.52 3.118e-12 695-708 PR00048A 10.52 3.647e-12 639-652 PR00048A 10.52 5.235e-12 611-624 PR00048A 10.52 7.882e-12 723-736 PR00048A 10.52 8.412e-12 443-456 PR00048A 10.52 5.737e-11 387-400 PR00048B 6.02 7.231e-11 627-636 PR00048A 10.52 8.105e-11 583-596 PR00048A 10.52 1.391e-10 303-316 PR00048B 6.02 1.563e-10 319-328 PR00048B 6.02 1.563e-10 739-748 PR00048B 6.02 2.125e-10 907-916 PR00048B 6.02 2.688e-10 431-440 PR00048B 6.02 2.688e-10 599-608 PR00048A 10.52 4.522e-10 471-484 PR00048B 6.02 5.500e-10 543-552 PR00048B 6.02 6.625e-10 711-720 PR00048B 6.02 7.750e-10 487-496 PR00048B 6.02 7.750e-10 683-692 PR00048A 10.52 9.217e-10 835-848 PR00048B 6.02 1.474e-09 879-888 PR00048B 6.02 1.947e-09 347-356 PR00048A 10.52 2.800e-09 667-680 PR00048B 6.02 5.737e-09 403-412 PR00048B 6.02 7.632e-09 515-524 PR00048B 6.02 8.105e-09 795-804 PR00048A 10.52 8.920e-09 275-288 PR00048B 6.02 9.526e-09 571-580 PR00048B 6.02 9.526e-09 767-776
1437	BL00579	Ribosomal protein L29 proteins.	BL00579B 21.99 5.065e-21 35-64
1439	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 3.432e-34 8-46
1439	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.235e-14 312-328 BL00028 16.07 6.294e-14 368-384 BL00028 16.07 7.882e-14 228-244 BL00028 16.07 4.150e-13 452-468 BL00028 16.07 5.304e-12 340-356 BL00028 16.07 6.478e-12 200-216 BL00028 16.07 8.435e-12 424-440 BL00028 16.07 9.217e-12 256-272 BL00028 16.07 1.692e-11 284-300 BL00028 16.07 5.154e-11 396-412

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Table 3

SEQ ID	Database entry ID	Description	Results*
			BL00028 16.07 9.654e-11 172-188
1439	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 1.818e-15 309-322 PR00048A 10.52 5.091e-15 225-238 PR00048A 10.52 4.750e-14 365-378 PR00048A 10.52 7.750e-14 169-182 PR00048A 10.52 2.929e-13 337-350 PR00048A 10.52 5.500e-13 253-266 PR00048A 10.52 6.786e-13 393-406 PR00048A 10.52 2.588e-12 281-294 PR00048A 10.52 4.176e-12 449-462 PR00048A 10.52 7.353e-12 421-434 PR00048B 6.02 1.692e-11 437-446 PR00048B 6.02 1.563e-10 241-250 PR00048B 6.02 2.688e-10 269-278 PR00048B 6.02 3.250e-10 353-362 PR00048B 6.02 4.375e-10 325-334 PR00048A 10.52 4.913e-10 197-210 PR00048B 6.02 4.316e-09 381-390
1439	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.800e-14 272-284 PD00066 13.92 2.800e-14 328-340 PD00066 13.92 6.400e-14 356-368 PD00066 13.92 2.000e-13 412-424 PD00066 13.92 3.500e-13 440-452 PD00066 13.92 6.500e-13 244-256 PD00066 13.92 1.857e-12 300-312 PD00066 13.92 5.286e-12 216-228 PD00066 13.92 8.286e-12 384-396 PD00066 13.92 5.200e-09 188-200
1446	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.500e-15 194-210 BL00028 16.07 3.118e-14 334-350 BL00028 16.07 1.000e-12 222-238 BL00028 16.07 6.478e-12 250-266 BL00028 16.07 9.217e-12 306-322 BL00028 16.07 9.217e-12 390-406 BL00028 16.07 1.000e-11 166-182 BL00028 16.07 6.192e-11 362-378 BL00028 16.07 9.654e-11 85-101 BL00028 16.07 2.200e-10 138-154 BL00028 16.07 6.400e-10 29-45 BL00028 16.07 7.600e-10 278-294
1446	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.500e-16 378-390 PD00066 13.92 9.100e-16 350-362 PD00066 13.92 5.154e-15 238-250 PD00066 13.92 2.800e-14 210-222 PD00066 13.92 3.143e-12 101-113 PD00066 13.92 3.143e-12 154-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			166 PD00066 13.92 8.714e-12 322-334 PD00066 13.92 9.143e-12 126-138 PD00066 13.92 9.143e-12 294-306 PD00066 13.92 1.000e-11 17-29 PD00066 13.92 9.217e-11 266-278 PD00066 13.92 1.346e-10 182-194 PD00066 13.92 4.462e-10 73-85 PD00066 13.92 5.200e-09 45-57
1446	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.000e-17 387-400 PR00048A 10.52 4.375e-16 191-204 PR00048A 10.52 7.750e-14 219-232 PR00048A 10.52 1.643e-13 331-344 PR00048A 10.52 3.571e-13 163-176 PR00048A 10.52 2.059e-12 359-372 PR00048A 10.52 2.588e-12 303-316 PR00048A 10.52 3.647e-12 82-95 PR00048A 10.52 7.353e-12 247-260 PR00048A 10.52 5.263e-11 275-288 PR00048B 6.02 5.846e-11 235-244 PR00048A 10.52 7.158e-11 26-39 PR00048A 10.52 1.783e-10 135-148 PR00048A 10.52 2.957e-10 54-67 PR00048B 6.02 5.500e-10 207-216 PR00048B 6.02 6.625e-10 347-356 PR00048B 6.02 8.875e-10 375-384 PR00048B 6.02 1.474e-09 179-188 PR00048B 6.02 1.474e-09 319-328 PR00048B 6.02 2.895e-09 70-79 PR00048B 6.02 5.737e-09 151-160
1451	PD02462	PROTEIN BOLA TRANSCRIPTION REGULATION AC.	PD02462A 22.48 9.658e-10 543-577
1451	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 4.375e-15 466-482 BL00028 16.07 6.063e-15 494-510 BL00028 16.07 6.063e-15 522-538 BL00028 16.07 4.706e-14 410-426 BL00028 16.07 5.500e-13 438-454 BL00028 16.07 7.750e-13 270-286 BL00028 16.07 9.100e-13 298-314 BL00028 16.07 2.731e-11 550-566 BL00028 16.07 5.500e-11 354-370 BL00028 16.07 5.500e-11 382-398 BL00028 16.07 1.300e-10 578-594 BL00028 16.07 3.100e-10 186-202 BL00028 16.07 7.600e-10 242-258 BL00028 16.07 2.800e-09 326-342 BL00028 16.07 4.086e-09 158-174

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Table 3

SEQ ID	Database entry ID	Description	Results*
1451	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.200e-14 314-326 PD00066 13.92 8.800e-14 230-242 PD00066 13.92 1.000e-13 482-494 PD00066 13.92 6.500e-13 510-522 PD00066 13.92 1.857e-12 258-270 PD00066 13.92 4.429e-12 286-298 PD00066 13.92 5.286e-12 398-410 PD00066 13.92 5.714e-12 454-466 PD00066 13.92 7.000e-12 370-382 PD00066 13.92 9.571e-12 174-186 PD00066 13.92 3.739e-11 566-578 PD00066 13.92 3.077e-10 202-214 PD00066 13.92 8.500e-09 426-438 PD00066 13.92 8.500e-09 538-550
1451	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 4.000e-14 407-420 PR00048A 10.52 2.929e-13 491-504 PR00048A 10.52 2.929e-13 519-532 PR00048A 10.52 5.500e-13 295-308 PR00048A 10.52 2.059e-12 267-280 PR00048A 10.52 2.588e-12 463-476 PR00048A 10.52 6.294e-12 575-588 PR00048A 10.52 7.882e-12 351-364 PR00048A 10.52 9.471e-12 379-392 PR00048A 10.52 9.526e-11 239-252 PR00048B 6.02 1.563e-10 423-432 PR00048A 10.52 4.522e-10 183-196 PR00048A 10.52 4.913e-10 323-336 PR00048B 6.02 6.063e-10 339-348 PR00048B 6.02 6.063e-10 535-544 PR00048B 6.02 8.313e-10 199-208 PR00048B 6.02 1.474e-09 311-320 PR00048B 6.02 3.842e-09 227-236 PR00048B 6.02 4.789e-09 171-180 PR00048A 10.52 4.960e-09 435-448 PR00048B 6.02 5.263e-09 507-516 PR00048A 10.52 7.480e-09 547-560 PR00048B 6.02 9.526e-09 283-292
1453	BL00354	HMG-I and HMG-Y DNA-binding domain proteins (A+T-hook).	BL00354A 3.83 1.000e-08 346-355
1454	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 1.300e-38 8-46
1454	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.000e-15 141-157 BL00028 16.07 1.450e-13 225-241 BL00028 16.07 3.250e-13 421-437 BL00028 16.07 4.150e-13 617-633 BL00028 16.07 9.100e-13 449-465 BL00028 16.07 9.100e-13 645-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			661 BL00028 16.07 4.130e-12 197-213 BL00028 16.07 9.217e-12 253-269 BL00028 16.07 1.346e-11 561-577 BL00028 16.07 4.115e-11 169-185 BL00028 16.07 4.462e-11 365-381 BL00028 16.07 5.154e-11 477-493 BL00028 16.07 5.154e-11 589-605 BL00028 16.07 1.300e-10 393-409 BL00028 16.07 2.500e-10 533-549 BL00028 16.07 4.900e-10 309-325 BL00028 16.07 5.500e-10 281-297 BL00028 16.07 5.500e-10 337-353 BL00028 16.07 7.000e-10 505-521
1454	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 4.462e-15 409-421 PD00066 13.92 4.462e-15 549-561 PD00066 13.92 4.462e-15 633-645 PD00066 13.92 5.846e-15 185-197 PD00066 13.92 8.615e-15 241-253 PD00066 13.92 2.800e-14 353-365 PD00066 13.92 2.800e-14 437-449 PD00066 13.92 2.800e-14 493-505 PD00066 13.92 2.800e-14 521-533 PD00066 13.92 2.800e-14 577-589 PD00066 13.92 2.800e-14 605-617 PD00066 13.92 5.800e-14 465-477 PD00066 13.92 8.200e-14 297-309 PD00066 13.92 2.000e-13 381-393 PD00066 13.92 4.000e-13 157-169 PD00066 13.92 5.500e-13 213-225 PD00066 13.92 3.348e-11 129-141 PD00066 13.92 6.870e-11 325-337 PD00066 13.92 3.400e-09 269-281
1454	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.875e-16 222-235 PR00048A 10.52 1.750e-14 194-207 PR00048A 10.52 2.500e-14 250-263 PR00048A 10.52 4.000e-14 138-151 PR00048A 10.52 7.000e-14 446-459 PR00048A 10.52 7.000e-14 586-599 PR00048A 10.52 7.000e-14 642-655 PR00048A 10.52 7.750e-14 362-375 PR00048A 10.52 9.250e-14 166-179 PR00048A 10.52 1.643e-13 558-571 PR00048A 10.52 5.500e-13 418-431 PR00048A 10.52 6.143e-13 474-487 PR00048A 10.52 6.143e-13 530-543 PR00048B 6.02 6.400e-13

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Table 3

SEQ ID	Database entry ID	Description	Results*
			434-443 PR00048A 10.52 1.000e-12 306-319 PR00048A 10.52 1.529e-12 614-627 PR00048A 10.52 2.059e-12 334- 347 PR00048B 6.02 1.000e-11 406-415 PR00048B 6.02 1.000e- 11 490-499 PR00048B 6.02 1.000e-11 574-583 PR00048B 6.02 1.692e-11 630-639 PR00048A 10.52 5.263e-11 390- 403 PR00048B 6.02 6.538e-11 602-611 PR00048B 6.02 7.231e- 11 238-247 PR00048B 6.02 7.231e-11 546-555 PR00048A 10.52 8.105e-11 502-515 PR00048B 6.02 2.688e-10 350- 359 PR00048B 6.02 3.813e-10 378-387 PR00048B 6.02 3.813e- 10 462-471 PR00048B 6.02 1.000e-09 294-303 PR00048B 6.02 2.895e-09 266-275 PR00048B 6.02 4.789e-09 210- 219 PR00048B 6.02 5.737e-09 518-527 PR00048B 6.02 9.526e- 09 182-191 PR00048B 6.02 1.000e-08 154-163
1455	BL00926	Lysyl oxidase copper-binding region proteins.	BL00926B 13.84 6.094e-09 457-494
1455	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 8.313e-15 400-416 BL00028 16.07 7.750e-13 87-103 BL00028 16.07 1.692e-11 285-301 BL00028 16.07 6.885e-11 59-75 BL00028 16.07 1.600e-10 313-329 BL00028 16.07 5.886e-09 115-131 BL00028 16.07 7.943e-09 245-261
1455	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.000e-09 416-428 PD00066 13.92 8.200e-09 75-87
1455	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 1.000e-10 84-97 PR00048A 10.52 4.130e-10 397-410 PR00048A 10.52 6.870e-10 282-295 PR00048A 10.52 8.920e-09 310-323
1457	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.300e-17 766-778 PD00066 13.92 7.231e-15 738-750 PD00066 13.92 2.800e-14 822-834 PD00066 13.92 5.200e-14 710-722 PD00066 13.92 3.739e-11 794-806
1457	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 8.650e-13 694-710 BL00028 16.07 4.130e-12 806-822 BL00028 16.07 4.462e-11 778-794 BL00028 16.07 8.615e-11 750-766 BL00028 16.07 1.600e-10 722-738

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Table 3

SEQ ID	Database entry ID	Description	Results*
			BL00028 16.07 4.000e-10 834-850
1457	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 6.051e-09 514-564
1457	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 3.250e-14 691-704 PR00048A 10.52 9.250e-14 775-788 PR00048A 10.52 5.500e-13 747-760 PR00048A 10.52 3.118e-12 803-816 PR00048A 10.52 7.353e-12 831-844 PR00048A 10.52 1.947e-11 719-732 PR00048B 6.02 4.462e-11 707-716 PR00048B 6.02 2.688e-10 763-772 PR00048B 6.02 5.500e-10 819-828 PR00048B 6.02 8.105e-09 735-744
1458	PR00041	CAMP RESPONSE ELEMENT BINDING (CREB) PROTEIN SIGNATURE	PR00041A 13.35 2.588e-28 56-78 PR00041B 8.61 1.000e-20 105-120
1459	DM00315	072 RIBONUCLEASE INHIBITOR.	DM00315G 15.85 3.430e-09 78-113
1462	PD01823	PROTEIN INTERGENIC REGION ABC1 PRECURSOR MITOCHONDRION T.	PD01823C 16.13 5.909e-14 214-234 PD01823B 14.96 1.655e-13 190-209 PD01823D 16.66 2.588e-09 292-312
1465	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 7.483e-09 772-825
1465	BL00795	Involucrin proteins.	BL00795C 17.06 9.700e-09 747-791
1466	PF00084	Sushi domain proteins (SCR repeat proteins).	PF00084B 9.45 9.100e-12 86-97 PF00084B 9.45 7.188e-10 263-274
1470	BL00021	Kringle domain proteins.	BL00021D 24.56 5.378e-31 55-96
1470	BL01253	Type I fibronectin domain proteins.	BL01253H 13.15 9.620e-22 65-99 BL01253G 11.34 2.149e-17 46-59
1470	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE	PR00722C 10.87 2.000e-16 46-58
1470	BL00495	Apple domain proteins.	BL00495N 11.04 2.414e-24 39-73 BL00495O 13.75 6.556e-14 74-102
1470	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134B 15.99 1.947e-20 47-70 BL00134C 13.45 5.875e-12 83-96
1471	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134B 15.99 7.857e-19 245-268 BL00134A 11.96 7.652e-18 89-105 BL00134C 13.45 5.200e-15 278-291
1471	BL01253	Type I fibronectin domain proteins.	BL01253G 11.34 3.961e-12 244-257 BL01253D 4.84 8.984e-12 89-102 BL01253H 13.15 3.406e-11 260-294
1471	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE	PR00722A 12.27 4.522e-16 90-105 PR00722C 10.87 3.045e-11 244-256 PR00722B 12.51 5.286e-10 144-158

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Table 3

SEQ ID	Database entry ID	Description	Results*
1471	BL00021	Kringle domain proteins.	BL00021B 13.33 8.929e-18 89-106 BL00021D 24.56 7.384e-09 250-291
1471	BL00495	Apple domain proteins.	BL00495O 13.75 2.385e-11 269-297 BL00495N 11.04 8.946e-09 237-271
1472	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 5.636e-10 419-439
1472	BL00410	Dynamin family proteins.	BL00410A 16.46 2.227e-09 414-453
1474	BL00113	Adenylate kinase proteins.	BL00113A 12.74 8.615e-09 596-612
1475	BL00113	Adenylate kinase proteins.	BL00113A 12.74 8.615e-09 553-569
1477	BL00690	DEAH-box subfamily ATP-dependent helicases proteins.	BL00690B 13.38 9.308e-19 144-161 BL00690A 6.87 1.000e-10 116-125
1477	BL00662	Bacterial type II secretion system protein E proteins.	BL00662D 8.67 5.553e-10 108-128
1478	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.652e-11 436-448
1478	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 9.526e-11 417-430 PR00048B 6.02 4.938e-10 433-442
1478	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 9.862e-10 108-117
1478	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 8.650e-13 420-436 BL00028 16.07 7.600e-10 392-408 BL00028 16.07 5.371e-09 478-494
1478	BL00826	MARCKS family proteins.	BL00826C 7.63 8.988e-09 89-115
1480	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.632e-11 278-291
1480	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 1.900e-09 269-281
1480	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 6.538e-11 281-297 BL00028 16.07 7.300e-10 239-255 BL00028 16.07 3.829e-09 434-450
1483	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 3.250e-10 194-226 DM00215 19.43 6.797e-09 246-278
1483	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 3.136e-09 213-227 PR00049D 0.00 3.136e-09 245-259 PR00049D 0.00 4.356e-09 215-229 PR00049D 0.00 4.356e-09 247-261 PR00049D 0.00 8.780e-09 212-226 PR00049D 0.00 8.780e-09 244-258 PR00049D 0.00 8.932e-09 211-225 PR00049D 0.00 8.932e-09 243-257
1485	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 6.644e-09 72-86
1486	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 4.190e-09 122-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			136
1488	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.750e-15 358-374
1488	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 1.000e-12 355-368 PR00048B 6.02 1.000e-11 343-352 PR00048B 6.02 5.737e-09 313-322
1488	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 9.308e-10 316-328 PD00066 13.92 7.600e-09 346-358
1488	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 8.892e-10 226-235 PR00308C 3.83 7.545e-09 225-234 PR00308A 5.90 8.200e-09 223-237
1488	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.500e-10 160-174 PR00049D 0.00 6.186e-09 159-173 PR00049D 0.00 9.237e-09 158-172
1489	BL00345	Ets-domain proteins.	BL00345B 21.28 5.154e-29 144-194
1489	DM00686	kw REPLICATION REP 28K 17.7K.	DM00686B 23.86 7.300e-12 160-206
1489	PR00454	ETS DOMAIN SIGNATURE	PR00454C 11.24 2.043e-11 158-176
1492	BL00559	Eukaryotic molybdopterin oxidoreductases proteins.	BL00559E 12.22 2.184e-09 1322-1346
1492	BL00652	TNFR/NGFR family cysteine-rich region proteins.	BL00652C 7.92 8.105e-09 882-892
1496	PR00625	DNAJ PROTEIN FAMILY SIGNATURE	PR00625A 12.84 5.385e-18 14-33 PR00625B 13.48 1.220e-17 46-66
1496	BL00636	Nt-dnaJ domain proteins.	BL00636B 15.11 8.500e-18 46-66 BL00636A 8.07 1.000e-16 18-34
1497	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.357e-30 252-294
1497	BL00032	'Homeobox' antennapedia-type protein.	BL00032C 11.28 4.563e-19 280-297 BL00032B 10.83 9.675e-15 241-279
1497	PR00024	HOMEBOX SIGNATURE	PR00024C 7.49 1.643e-13 284-293 PR00024B 11.27 5.846e-13 274-284
1497	PR00031	LAMBDA AND OTHER REPRESSOR HELIX-TURN-HELIX SIGNATURE	PR00031B 16.29 2.440e-11 275-291
1497	DM01724	kw ALLERGEN POLLEN CIM1 HOL-LI.	DM01724 8.14 2.421e-09 77-96
1497	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.143e-10 191-205 PR00049D 0.00 8.786e-10 184-198 PR00049D 0.00 2.983e-09 187-201
1497	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 8.892e-10 108-117 PR00308C 3.83 8.892e-10 109-118 PR00308C 3.83 8.892e-10 110-119 PR00308C 3.83 8.892e-10 111-120 PR00308A 5.90 5.553e-09 107-121
1501	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.438e-28 97-139
1501	BL00032	'Homeobox' antennapedia-type protein.	BL00032B 10.83 9.024e-15 86-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			124 BL00032C 11.28 5.235e-12 125-142
1501	PR00025	HOMEOTIC ANTENNAPEDIA PROTEIN SIGNATURE	PR00025B 11.94 8.714e-12 83-98
1501	PR00026	ENGRAILED HOMEODOMAIN SIGNATURE	PR00026A 7.47 6.271e-10 81-98
1501	PR00028	POU DOMAIN SIGNATURE	PR00028D 17.92 5.000e-09 81-101
1501	PR00024	HOMEODOMAIN SIGNATURE	PR00024C 7.49 4.273e-11 129-138 PR00024B 11.27 1.000e-08 119-129
1508	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.500e-28 31-73
1508	PR00031	LAMBDA AND OTHER REPRESSOR HELIX-TURN-HELIX SIGNATURE	PR00031B 16.29 8.714e-17 54-70
1508	PR00024	HOMEODOMAIN SIGNATURE	PR00024C 7.49 1.750e-14 63-72 PR00024B 11.27 9.000e-11 53-63
1508	BL00032	'Homeobox' antennapedia-type protein.	BL00032C 11.28 8.393e-16 59-76 BL00032B 10.83 2.710e-10 20-58
1511	BL00048	Protamine P1 proteins.	BL00048 6.39 7.300e-09 140-166
1512	PF00624	Flocculin repeat proteins.	PF00624I 9.10 3.480e-09 670-699
1512	PR00487	FILAGGRIN SIGNATURE	PR00487I 5.13 8.159e-09 689-708
1512	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 8.953e-10 668-716 BL00115Z 3.12 7.154e-09 661-709 BL00115Z 3.12 9.074e-09 670-718
1513	PR00348	UBIQUITIN SIGNATURE	PR00348C 20.03 7.107e-17 80-101 PR00348B 5.78 7.254e-16 59-79 PR00348A 7.86 1.679e-14 38-58
1513	BL00299	Ubiquitin domain proteins.	BL00299 28.84 4.600e-13 43-94
1514	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 7.750e-15 1686-1719
1514	PF00856	SET domain proteins.	PF00856B 16.42 8.875e-18 1668-1689 PF00856A 26.14 2.909e-14 1614-1650
1514	PF00855	PWWP domain proteins.	PF00855 13.75 7.300e-11 1419-1435
1514	PF00628	PHD-finger.	PF00628 15.84 3.893e-10 1383-1397
1514	DM00552	GROWTH FACTOR AND CYTOKINES RECEPTORS FAMILY.	DM00552C 24.30 8.324e-09 1611-1658
1514	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 9.679e-09 1379-1394
1519	BL01282	BIR repeat proteins.	BL01282B 30.49 9.036e-13 912-950
1525	PD01876	ANTIGEN MELANOMA-ASSOCIATED MULTIGENE FAMILY TUM.	PD01876C 21.73 9.481e-11 38-90
1526	BL00191	Cytochrome b5 family, heme-binding domain proteins.	BL00191K 17.38 9.308e-11 189-232 BL00191I 14.64 5.755e-10 118-132
1526	PR00410	PHENOL HYDROXYLASE REDUCTASE FAMILY SIGNATURE	PR00410D 12.97 1.761e-09 185-204
1526	PR00371	FLAVOPROTEIN PYRIDINE NUCLEOTIDE CYTOCHROME REDUCTASE SIGNATURE	PR00371D 14.55 4.000e-09 185-204

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Table 3

SEQ ID	Database entry ID	Description	Results*
1526	PR00406	CYTOCHROME B5 REDUCTASE SIGNATURE	PR00406B 9.00 3.432e-09 126-133 PR00406D 10.02 8.200e-09 185-204
1527	PD01234	PROTEIN NUCLEAR BROMODOMAIN TRANS.	PD01234B 15.53 9.357e-09 707-724
1528	PD01234	PROTEIN NUCLEAR BROMODOMAIN TRANS.	PD01234B 15.53 9.357e-09 789-806
1529	BL00784	Ribosomal protein L34 proteins.	BL00784 14.98 1.920e-09 18-55
1529	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 8.405e-09 16-35
1529	BL00048	Protamine P1 proteins.	BL00048 6.39 1.969e-13 14-40 BL00048 6.39 3.515e-12 24-50 BL00048 6.39 4.838e-12 27-53 BL00048 6.39 5.368e-12 30-56 BL00048 6.39 5.500e-12 2-28 BL00048 6.39 6.559e-12 12-38 BL00048 6.39 8.676e-12 4-30 BL00048 6.39 2.375e-11 34-60 BL00048 6.39 3.125e-11 33-59 BL00048 6.39 4.500e-11 6-32 BL00048 6.39 4.625e-11 25-51 BL00048 6.39 4.750e-11 29-55 BL00048 6.39 6.000e-11 31-57 BL00048 6.39 6.375e-11 28-54 BL00048 6.39 7.500e-11 26-52 BL00048 6.39 8.625e-11 36-62 BL00048 6.39 9.750e-11 32-58 BL00048 6.39 9.875e-11 16-42 BL00048 6.39 3.368e-10 22-48 BL00048 6.39 4.434e-10 23-49 BL00048 6.39 4.789e-10 35-61 BL00048 6.39 6.921e-10 15-41 BL00048 6.39 9.053e-10 38-64 BL00048 6.39 1.900e-09 18-44 BL00048 6.39 2.013e-09 20-46 BL00048 6.39 2.238e-09 37-63 BL00048 6.39 2.913e-09 10-36 BL00048 6.39 2.913e-09 39-65 BL00048 6.39 5.613e-09 8-34 BL00048 6.39 9.100e-09 11-37
1529	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301B 5.49 9.654e-09 330-340
1532	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 9.571e-12 310-322
1532	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 4.051e-09 750-764
1532	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 4.429e-09 926-938
1532	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.300e-10 711-727 BL00028 16.07 6.143e-09 1002-1018
1532	BL00291	Prion protein.	BL00291A 4.49 7.517e-09 781-815
1532	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 8.322e-09 944-976

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Table 3

SEQ ID	Database entry ID	Description	Results*
1534	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 7.568e-22 834-874 PD00930A 25.62 8.977e-13 731-756
1534	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405A 17.71 6.625e-12 307-326 PR00405B 11.83 3.318e-09 326-343
1534	PF00620	GTPase-activator protein for Rho-like GTPases.	PF00620B 14.20 3.357e-09 783-799
1535	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 7.568e-22 834-874 PD00930A 25.62 8.977e-13 731-756
1535	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405A 17.71 6.625e-12 307-326 PR00405B 11.83 3.318e-09 326-343
1535	PF00620	GTPase-activator protein for Rho-like GTPases.	PF00620B 14.20 3.357e-09 783-799
1536	BL00274	Aerolysin type toxins proteins.	BL00274C 22.24 8.340e-09 121-170
1537	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301A 10.24 7.300e-09 378-388 PD00301A 10.24 1.000e-08 377-387
1541	BL00936	Ribosomal protein L35 proteins.	BL00936A 11.46 5.787e-15 2-20
1541	PR00064	RIBOSOMAL PROTEIN L35 SIGNATURE	PR00064B 13.11 3.432e-14 21-35 PR00064A 9.98 7.623e-14 3-20 PR00064C 14.65 3.204e-13 36-54
1547	BL00415	Synapsins proteins.	BL00415P 2.37 9.069e-09 735-770
1556	PR00345	STATHMIN FAMILY SIGNATURE	PR00345B 7.12 5.458e-09 297-325
1556	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 9.471e-09 192-207
1557	PR00345	STATHMIN FAMILY SIGNATURE	PR00345B 7.12 6.551e-09 297-325
1557	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 6.824e-09 192-207
1557	BL00240	Receptor tyrosine kinase class III proteins.	BL00240F 17.74 7.750e-09 163-210
1557	PF00992	Troponin.	PF00992A 16.67 9.053e-09 310-344
1559	DM01871	kw SSR LIGASE CYCLO FORMYLTETRAHYDROFOLATE.	DM01871B 16.47 4.622e-10 135-163
1563	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00720B 16.57 4.103e-18 1401-1424
1563	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 4.326e-16 689-711
1564	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00720B 16.57 4.103e-18 1089-1112
1564	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 4.326e-16 377-399
1569	BL00540	Ferritin iron-binding regions proteins.	BL00540B 18.82 1.000e-40 258-312 BL00540B 18.82 4.960e-34 138-192 BL00540A 15.06 5.255e-27 47-87
1570	PF00084	Sushi domain proteins (SCR repeat proteins).	PF00084B 9.45 4.150e-09 67-78

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Table 3

SEQ ID	Database entry ID	Description	Results*
1572	BL01113	C1q domain proteins.	BL01113A 17.99 4.255e-10 578-604
1572	DM01891	TYB PROTEIN.	DM01891B 5.05 8.278e-09 123-154
1572	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 2.571e-10 206-220 PR00049D 0.00 7.407e-09 581-595 PR00049D 0.00 9.085e-09 567-581
1573	BL00299	Ubiquitin domain proteins.	BL00299 28.84 4.600e-26 14-65
1577	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 5.737e-20 42-59 PR00405A 17.71 2.703e-17 23-42 PR00405C 19.41 6.902e-10 63-84
1578	PD01234	PROTEIN NUCLEAR BROMODOMAIN TRANS.	PD01234B 15.53 4.750e-10 355-372
1579	BL00226	Intermediate filaments proteins.	BL00226B 23.86 3.182e-28 189-236 BL00226D 19.10 8.096e-21 355-401 BL00226C 13.23 2.333e-20 254-284 BL00226A 12.77 6.400e-17 85-99
1579	PR00486	UTEROGLOBIN SIGNATURE	PR00486C 14.71 9.379e-10 331-348
1582	BL00273	Heat-stable enterotoxins proteins.	BL00273 12.24 7.638e-10 125-137
1582	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 1.191e-10 52-97 BL00203 13.94 2.194e-09 90-135 BL00203 13.94 3.204e-09 47-92
1582	BL01138	Scorpion short toxins proteins.	BL01138A 10.96 9.372e-09 37-48
1583	BL01215	Mrp family proteins.	BL01215C 18.97 1.000e-40 119-160 BL01215D 30.07 1.000e-40 178-227 BL01215A 9.75 6.344e-26 53-79
1583	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 4.103e-09 56-77
1583	PR00091	NITROGENASE COMPONENT II SIGNATURE	PR00091A 8.10 4.945e-09 61-74
1583	PR00364	DISEASE RESISTANCE PROTEIN SIGNATURE	PR00364A 8.19 9.080e-09 57-72
1585	BL00225	Crystallins beta and gamma 'Greek key' motif proteins.	BL00225B 18.06 8.650e-31 54-88 BL00225B 18.06 8.297e-20 143-177 BL00225B 18.06 6.878e-15 234-268 BL00225A 13.82 4.732e-12 15-35 BL00225B 18.06 2.887e-11 324-358 BL00225B 18.06 4.000e-09 8-42
1586	PR00359	B-CLASS P450 SIGNATURE	PR00359C 14.07 3.250e-09 63-78
1587	BL01283	T-box domain proteins.	BL01283B 23.17 1.545e-33 30-71 BL01283D 11.70 1.000e-32 116-148 BL01283C 13.05 7.857e-17 82-95
1587	PR00937	T-BOX DOMAIN SIGNATURE	PR00937D 13.41 3.700e-18 81-95 PR00937E 11.86 9.471e-17 119-132 PR00937B 14.58 4.900e-14 45-58 PR00937C 10.51 3.400e-12 62-71 PR00937F 12.53 4.103e-11 140-148

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Table 3

SEQ ID	Database entry ID	Description	Results*
1590	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456F 5.86 1.000e-10 87-98
1591	PR00370	FLAVIN-CONTAINING MONOOXYGENASE (FMO) SIGNATURE	PR00370G 10.45 9.182e-25 537-558 PR00370B 10.91 1.000e-21 74-92 PR00370D 16.33 3.893e-21 232-250 PR00370C 12.72 7.500e-20 187-203 PR00370E 11.96 1.563e-18 380-398 PR00370A 3.35 6.484e-12 51-66 PR00370F 17.75 8.809e-12 435-454
1591	PR00469	PYRIDINE NUCLEOTIDE DISULPHIDE REDUCTASE CLASS-II SIGNATURE	PR00469F 16.51 9.609e-11 229-253
1591	BL00677	D-amino acid oxidases proteins.	BL00677A 6.96 3.687e-09 51-63
1591	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 5.600e-09 53-84
1591	PR00368	FAD-DEPENDENT PYRIDINE NUCLEOTIDE REDUCTASE SIGNATURE	PR00368C 15.74 6.526e-10 233-258 PR00368A 17.76 5.982e-09 51-73
1591	PR00420	AROMATIC-RING HYDROXYLASE (FLAVOPROTEIN MONOOXYGENASE) SIGNATURE	PR00420A 14.78 8.377e-10 233-255 PR00420A 14.78 7.955e-09 51-73
1592	PR00370	FLAVIN-CONTAINING MONOOXYGENASE (FMO) SIGNATURE	PR00370G 10.45 9.182e-25 575-596 PR00370B 10.91 1.000e-21 112-130 PR00370D 16.33 3.893e-21 270-288 PR00370C 12.72 7.500e-20 225-241 PR00370E 11.96 1.563e-18 418-436 PR00370A 3.35 6.484e-12 89-104 PR00370F 17.75 8.809e-12 473-492
1592	PR00469	PYRIDINE NUCLEOTIDE DISULPHIDE REDUCTASE CLASS-II SIGNATURE	PR00469F 16.51 9.609e-11 267-291
1592	BL00677	D-amino acid oxidases proteins.	BL00677A 6.96 3.687e-09 89-101
1592	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 5.600e-09 91-122
1592	PR00368	FAD-DEPENDENT PYRIDINE NUCLEOTIDE REDUCTASE SIGNATURE	PR00368C 15.74 6.526e-10 271-296 PR00368A 17.76 5.982e-09 89-111
1592	PR00420	AROMATIC-RING HYDROXYLASE (FLAVOPROTEIN MONOOXYGENASE) SIGNATURE	PR00420A 14.78 8.377e-10 271-293 PR00420A 14.78 7.955e-09 89-111
1593	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.	BL00319C 17.12 9.500e-10 366-399
1594	BL00027	'Homeobox' domain proteins.	BL00027 26.43 2.895e-24 206-248
1594	PR00031	LAMBDA AND OTHER REPRESSOR HELIX-TURN-HELIX SIGNATURE	PR00031B 16.29 9.609e-12 229-245
1594	BL00478	LIM domain proteins.	BL00478B 14.79 9.250e-17 110-124 BL00478B 14.79 4.200e-11 48-62
1594	BL00032	'Homeobox' antennapedia-type protein.	BL00032C 11.28 2.581e-10 234-251
1594	BL00035	'POU' domain proteins.	BL00035C 17.40 2.962e-10 213-242
1594	PR00024	HOMEBOX SIGNATURE	PR00024C 7.49 7.900e-09 238-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			247
1596	PD02316	RNA POLYMERASE NUCLEOCAPSID ALPHA SUBUNIT RNA-D.	PD02316B 25.30 8.515e-09 1031-1085
1600	BL00353	HMG1/2 proteins.	BL00353B 11.47 3.089e-12 1310-1359
1600	BL00633	Bromodomain proteins.	BL00633B 13.82 1.000e-16 556-580 BL00633B 13.82 3.032e-16 218-242 BL00633B 13.82 5.886e-15 694-718 BL00633B 13.82 7.975e-13 418-442 BL00633B 13.82 9.325e-13 82-106 BL00633C 15.24 4.522e-10 451-463
1600	PR00503	BROMODOMAIN SIGNATURE	PR00503D 20.81 6.760e-17 589-608 PR00503B 9.96 5.655e-16 555-571 PR00503B 9.96 9.182e-15 217-233 PR00503B 9.96 1.973e-14 693-709 PR00503D 20.81 7.000e-13 251-270 PR00503D 20.81 8.154e-13 451-470 PR00503D 20.81 3.045e-12 727-746 PR00503B 9.96 7.660e-11 81-97 PR00503C 19.84 6.860e-10 571-589
1600	BL00415	Synapsins proteins.	BL00415N 4.29 8.500e-11 1456-1499 BL00415N 4.29 9.212e-09 1449-1492
1600	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301B 5.49 9.654e-09 915-925
1601	PR00409	PHTHALATE DIOXYGENASE REDUCTASE FAMILY SIGNATURE	PR00409D 13.02 8.544e-09 102-116
1604	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.831e-23 48-86
1604	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.600e-14 316-328 PD00066 13.92 2.000e-13 372-384 PD00066 13.92 4.000e-13 428-440 PD00066 13.92 5.000e-13 344-356 PD00066 13.92 5.000e-13 512-524 PD00066 13.92 8.000e-13 540-552 PD00066 13.92 8.500e-13 456-468 PD00066 13.92 3.571e-12 400-412 PD00066 13.92 9.571e-12 288-300 PD00066 13.92 3.700e-09 484-496
1604	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 6.625e-16 521-534 PR00048A 10.52 6.727e-15 409-422 PR00048A 10.52 8.364e-15 381-394 PR00048A 10.52 4.750e-14 353-366 PR00048A 10.52 1.643e-13 437-450 PR00048A 10.52 1.643e-13 465-478 PR00048A 10.52 6.786e-13 325-338 PR00048A 10.52 1.474e-11 549-562 PR00048B 6.02 6.063e-10 509-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			518 PR00048B 6.02 8.313e-10 537-546 PR00048A 10.52 9.217e-10 493-506 PR00048B 6.02 9.438e-10 397-406 PR00048B 6.02 9.438e-10 481- 490 PR00048B 6.02 2.895e-09 369-378 PR00048A 10.52 3.880e-09 297-310
1604	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.350e-13 412- 428 BL00028 16.07 2.350e-13 524-540 BL00028 16.07 6.400e- 13 468-484 BL00028 16.07 2.565e-12 356-372 BL00028 16.07 3.348e-12 328-344 BL00028 16.07 3.739e-12 496- 512 BL00028 16.07 4.808e-11 384-400 BL00028 16.07 2.500e- 10 440-456 BL00028 16.07 6.100e-10 272-288 BL00028 16.07 7.900e-10 552-568 BL00028 16.07 4.343e-09 300- 316
1609	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 3.250e-11 168- 181 PR00019A 11.19 4.130e-10 263-276 PR00019A 11.19 8.043e-10 58-71 PR00019B 11.36 8.200e-10 260-273 PR00019A 11.19 4.000e-09 121-134 PR00019A 11.19 6.667e-09 286- 299 PR00019B 11.36 7.480e-09 55-68
1609	BL00868	Cys/Met metabolism enzymes pyridoxal-phosphate attachment sit.	BL00868D 24.35 9.250e-09 654- 696
1609	PR00597	GELSOLIN FAMILY SIGNATURE	PR00597G 8.55 6.333e-19 1207- 1229 PR00597B 9.78 3.526e-12 944-960 PR00597G 8.55 4.162e- 12 787-809 PR00597A 12.96 4.094e-11 837-858 PR00597B 9.78 4.818e-10 533-549 PR00597F 16.29 3.219e-09 710- 729 PR00597C 14.19 4.125e-09 559-577 PR00597E 13.46 5.192e- 09 1088-1108 PR00597G 8.55 9.791e-09 654-676
1611	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.059e-14 74-90
1611	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 1.000e-13 62-74
1611	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 6.143e-13 71-84 PR00048B 6.02 6.538e-11 59-68
1614	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 4.652e-14 38-69
1614	BL00076	Pyridine nucleotide-disulphide oxidoreductases class-I.	BL00076A 18.83 9.043e-12 35-64
1614	BL01280	Glucose inhibited division protein A family proteins.	BL01280A 15.97 1.766e-10 36-76
1614	PR00419	ADRENODOXIN REDUCTASE FAMILY	PR00419A 14.89 3.531e-10 36-58

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Table 3

SEQ ID	Database entry ID	Description	Results*
		SIGNATURE	
1614	PR00420	AROMATIC-RING HYDROXYLASE (FLAVOPROTEIN MONOOXYGENASE) SIGNATURE	PR00420A 14.78 4.393e-10 36-58
1614	BL00504	Fumarate reductase / succinate dehydrogenase FAD-binding site proteins.	BL00504A 10.76 7.041e-10 36-57
1614	BL00623	GMC oxidoreductases proteins.	BL00623A 12.60 4.086e-09 36-54
1614	PR00469	PYRIDINE NUCLEOTIDE DISULPHIDE REDUCTASE CLASS-II SIGNATURE	PR00469A 15.46 4.462e-09 36-58
1614	PR00368	FAD-DEPENDENT PYRIDINE NUCLEOTIDE REDUCTASE SIGNATURE	PR00368A 17.76 3.942e-10 36-58 PR00368C 15.74 9.115e-09 36-61
1614	BL00747	Glutamyl-tRNA reductase proteins.	BL00747E 19.60 1.000e-08 37-71
1615	PR00939	C2HC-TYPE ZINC-FINGER SIGNATURE	PR00939B 13.27 2.059e-09 610-618 PR00939A 8.95 4.682e-09 1051-1060
1615	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301A 10.24 7.300e-09 488-498
1617	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 2.915e-11 77-101
1621	PR00382	PLANT PHOSPHOLIPID TRANSFER PROTEIN SIGNATURE ^o	PR00382B 9.32 5.600e-09 31-45
1622	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380D 9.93 5.500e-24 307-328 PR00380A 14.18 3.864e-19 100-121 PR00380B 12.64 6.657e-15 221-238 PR00380C 13.18 7.900e-15 255-273
1622	BL00411	Kinesin motor domain proteins.	BL00411H 15.66 2.688e-32 306-336 BL00411G 21.39 5.781e-27 256-297 BL00411C 15.04 6.000e-22 100-121 BL00411F 14.77 2.575e-17 212-236 BL00411E 10.43 8.953e-13 149-167 BL00411B 13.51 5.500e-11 66-82 BL00411A 11.31 8.535e-09 7-21
1623	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320B 12.19 5.935e-11 428-442 PR00320A 16.74 6.897e-11 428-442 PR00320C 13.01 7.652e-11 428-442 PR00320B 12.19 2.125e-09 799-813
1623	PF00913	Trypanosome variant surface glycoprotein.	PF00913A 7.33 2.500e-09 1171-1177
1623	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 9.053e-09 430-440
1624	BL00633	Bromodomain proteins.	BL00633B 13.82 5.500e-11 80-104
1624	PR00503	BROMODOMAIN SIGNATURE	PR00503D 20.81 1.931e-09 113-132
1625	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.800e-14 374-386 PD00066 13.92 5.500e-13 743-755
1625	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 5.304e-10 752-765 PR00048B 6.02 7.750e-10 740-749 PR00048A 10.52 8.043e-10 383-396 PR00048B

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Table 3

SEQ ID	Database entry ID	Description	Results*
			6.02 3.368e-09 371-380
1625	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301A 10.24 6.400e-09 462-472
1625	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.565e-12 358-374 BL00028 16.07 6.870e-12 727-743 BL00028 16.07 9.229e-09 152-168
1625	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 1.000e-08 320-352
1630	PR00742	GLYCOSYL HYDROLASE FAMILY 35 SIGNATURE	PR00742I 13.54 5.875e-14 200-216
1630	BL01182	Glycosyl hydrolases family 35 proteins.	BL01182F 10.07 2.980e-13 200-214
1631	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 5.941e-27 31-69
1631	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.800e-16 279-291 PD00066 13.92 5.800e-14 307-319 PD00066 13.92 7.600e-14 223-235 PD00066 13.92 7.000e-13 335-347 PD00066 13.92 9.500e-13 251-263 PD00066 13.92 1.000e-12 195-207 PD00066 13.92 1.857e-12 363-375
1631	BL00466	TFIIS zinc ribbon domain proteins.	BL00466 25.88 6.609e-10 263-299
1631	BL01030	RNA polymerases M / 15 Kd subunits proteins.	BL01030 23.44 9.880e-10 263-300
1631	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.550e-13 375-391 BL00028 16.07 1.783e-12 207-223 BL00028 16.07 5.500e-11 319-335 BL00028 16.07 6.192e-11 291-307 BL00028 16.07 8.962e-11 179-195 BL00028 16.07 2.500e-10 263-279 BL00028 16.07 4.000e-10 235-251 BL00028 16.07 8.200e-10 347-363 BL00028 16.07 7.943e-09 151-167
1631	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 4.214e-13 204-217 PR00048A 10.52 5.500e-13 372-385 PR00048A 10.52 2.059e-12 232-245 PR00048A 10.52 8.941e-12 176-189 PR00048A 10.52 6.684e-11 316-329 PR00048A 10.52 1.391e-10 288-301 PR00048B 6.02 4.375e-10 276-285 PR00048A 10.52 8.435e-10 344-357 PR00048B 6.02 1.947e-09 304-313 PR00048A 10.52 5.680e-09 260-273 PR00048B 6.02 8.105e-09 220-229
1637	BL01283	T-box domain proteins.	BL01283D 11.70 1.675e-30 131-163 BL01283B 23.17 4.273e-20 42-83 BL01283C 13.05 4.073e-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			14 94-107
1637	PR00937	T-BOX DOMAIN SIGNATURE	PR00937D 13.41 3.919e-15 93-107 PR00937E 11.86 5.378e-14 134-147 PR00937B 14.58 4.176e-13 57-70 PR00937F 12.53 1.450e-12 155-163 PR00937C 10.51 4.938e-10 74-83
1637	PR00938	BRACHYURY PROTEIN FAMILY SIGNATURE	PR00938C 8.28 2.674e-09 98-115
1640	BL00027	'Homeobox' domain proteins.	BL00027 26.43 2.688e-28 132-174
1640	PR00031	LAMBDA AND OTHER REPRESSOR HELIX-TURN-HELIX SIGNATURE	PR00031B 16.29 1.643e-17 155-171
1640	BL00032	'Homeobox' antennapedia-type protein.	BL00032C 11.28 2.220e-15 160-177 BL00032B 10.83 6.516e-12 121-159
1640	PR00024	HOMEODOMAIN SIGNATURE	PR00024B 11.27 8.800e-12 154-164 PR00024C 7.49 3.769e-10 164-173
1640	PR00026	ENGRAILED HOMEODOMAIN SIGNATURE	PR00026A 7.47 3.520e-09 116-133
1644	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.	BL00319C 17.12 1.592e-09 486-519
1644	DM01724	kw ALLERGEN POLLEN CIM1 HOL-LI.	DM01724 8.14 5.855e-09 26-45
1645	BL00027	'Homeobox' domain proteins.	BL00027 26.43 2.800e-19 30-72 BL00027 26.43 5.645e-16 116-158
1645	PR00024	HOMEODOMAIN SIGNATURE	PR00024C 7.49 5.500e-10 62-71
1645	BL00032	'Homeobox' antennapedia-type protein.	BL00032C 11.28 8.662e-10 58-75
1646	BL00799	Granulins proteins.	BL00799F 13.26 4.957e-09 129-181
1646	PD02283	PROTEIN SPORULATION REPEAT PRECU.	PD02283C 17.54 6.063e-09 98-125
1646	BL00273	Heat-stable enterotoxins proteins.	BL00273 12.24 7.536e-09 156-168
1646	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 7.033e-11 106-151 BL00203 13.94 9.110e-11 81-126 BL00203 13.94 3.298e-10 146-191 BL00203 13.94 6.936e-10 130-175 BL00203 13.94 8.755e-10 167-212 BL00203 13.94 1.551e-09 101-146 BL00203 13.94 2.102e-09 127-172 BL00203 13.94 2.469e-09 200-245 BL00203 13.94 6.235e-09 208-253 BL00203 13.94 7.704e-09 63-108 BL00203 13.94 8.347e-09 182-227
1647	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 4.462e-27 98-151 BL01160B 19.54 3.382e-25 91-144 BL01160A 15.67 9.778e-15 18-56
1647	PR00381	KINESIN LIGHT CHAIN SIGNATURE	PR00381A 9.55 7.429e-14 107-124
1647	PR00194	TROPOMYOSIN SIGNATURE	PR00194D 9.57 5.690e-11 122-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			145
1649	BL00353	HMG1/2 proteins.	BL00353B 11.47 2.559e-09 83-132
1651	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.000e-14 214-226 PD00066 13.92 4.808e-10 119-131 PD00066 13.92 5.154e-10 242-254
1651	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.846e-11 198-214 BL00028 16.07 4.000e-10 254-270 BL00028 16.07 1.000e-09 226-242
1651	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 4.176e-12 223-236 PR00048A 10.52 1.720e-09 195-208 PR00048A 10.52 3.880e-09 251-264
1652	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 4.462e-15 398-410 PD00066 13.92 4.462e-15 762-774 PD00066 13.92 2.800e-14 370-382 PD00066 13.92 2.800e-14 426-438 PD00066 13.92 2.800e-14 482-494 PD00066 13.92 2.800e-14 538-550 PD00066 13.92 2.800e-14 650-662 PD00066 13.92 2.800e-14 678-690 PD00066 13.92 2.800e-14 818-830 PD00066 13.92 2.800e-14 846-858 PD00066 13.92 5.200e-14 594-606 PD00066 13.92 5.800e-14 622-634 PD00066 13.92 5.500e-13 454-466 PD00066 13.92 5.500e-13 706-718 PD00066 13.92 8.500e-13 510-522 PD00066 13.92 1.783e-11 790-802 PD00066 13.92 2.957e-11 734-746 PD00066 13.92 5.304e-11 342-354
1652	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.450e-13 802-818 BL00028 16.07 2.350e-13 276-292 BL00028 16.07 5.950e-13 858-874 BL00028 16.07 1.000e-12 830-846 BL00028 16.07 6.087e-12 606-622 BL00028 16.07 7.652e-12 382-398 BL00028 16.07 8.043e-12 718-734 BL00028 16.07 9.609e-12 354-370 BL00028 16.07 9.609e-12 774-790 BL00028 16.07 1.692e-11 746-762 BL00028 16.07 3.077e-11 662-678 BL00028 16.07 3.423e-11 690-706 BL00028 16.07 5.846e-11 522-538 BL00028 16.07 1.000e-10 550-566 BL00028 16.07 1.300e-10 410-426 BL00028 16.07 2.200e-10 634-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			650 BL00028 16.07 2.500e-10 438-454 BL00028 16.07 2.800e-10 494-510 BL00028 16.07 3.700e-10 578-594 BL00028 16.07 7.000e-10 466-482
1652	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 2.500e-14 855-868 PR00048A 10.52 5.500e-14 827-840 PR00048A 10.52 7.000e-14 603-616 PR00048A 10.52 9.250e-14 743-756 PR00048A 10.52 2.286e-13 659-672 PR00048A 10.52 5.235e-12 687-700 PR00048A 10.52 7.353e-12 379-392 PR00048A 10.52 8.941e-12 799-812 PR00048A 10.52 1.000e-11 351-364 PR00048A 10.52 1.947e-11 631-644 PR00048A 10.52 2.421e-11 715-728 PR00048A 10.52 3.368e-11 491-504 PR00048A 10.52 3.842e-11 407-420 PR00048B 6.02 4.462e-11 787-796 PR00048B 6.02 4.462e-11 843-852 PR00048B 6.02 5.154e-11 367-376 PR00048B 6.02 5.154e-11 423-432 PR00048B 6.02 5.154e-11 507-516 PR00048A 10.52 6.211e-11 463-476 PR00048A 10.52 6.211e-11 547-560 PR00048B 6.02 7.231e-11 479-488 PR00048A 10.52 8.105e-11 771-784 PR00048B 6.02 1.563e-10 647-656 PR00048B 6.02 2.125e-10 535-544 PR00048B 6.02 2.125e-10 675-684 PR00048A 10.52 3.348e-10 435-448 PR00048A 10.52 3.348e-10 519-532 PR00048B 6.02 4.938e-10 815-824 PR00048B 6.02 7.188e-10 591-600 PR00048B 6.02 8.313e-10 451-460 PR00048B 6.02 8.313e-10 703-712 PR00048B 6.02 8.875e-10 395-404 PR00048A 10.52 1.000e-09 273-286 PR00048B 6.02 4.316e-09 563-572 PR00048B 6.02 7.158e-09 619-628 PR00048B 6.02 1.000e-08 289-298
1656	PD01876	ANTIGEN MELANOMA-ASSOCIATED MULTIGENE FAMILY TUM.	PD01876C 21.73 3.438e-13 157-209
1660	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 6.444e-10 172-184
1660	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.790e-11 227-241 PR00049D 0.00 9.929e-10 228-242 PR00049D 0.00 3.746e-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			09 117-131
1660	PD02059	CORE POLYPROTEIN PROTEIN GAG CONTAINS: P.	PD02059B 24.48 8.732e-09 226-260
1660	BL00415	Synapsins proteins.	BL00415N 4.29 7.143e-11 80-123 BL00415N 4.29 5.260e-10 119-162 BL00415Q 2.23 6.959e-09 160-195 BL00415N 4.29 9.474e-09 72-115
1660	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 9.695e-09 234-266
1661	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.077e-15 211-223 PD00066 13.92 3.077e-15 379-391 PD00066 13.92 3.077e-15 407-419 PD00066 13.92 3.077e-15 435-447 PD00066 13.92 3.400e-14 519-531 PD00066 13.92 3.500e-13 351-363 PD00066 13.92 4.000e-13 239-251 PD00066 13.92 6.087e-11 323-335 PD00066 13.92 6.870e-11 295-307 PD00066 13.92 9.609e-11 267-279
1661	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 1.643e-13 528-541 PR00048A 10.52 2.286e-13 220-233 PR00048A 10.52 6.786e-13 304-317 PR00048B 6.02 1.000e-12 376-385 PR00048B 6.02 1.000e-12 432-441 PR00048A 10.52 3.647e-12 276-289 PR00048B 6.02 5.000e-12 208-217 PR00048A 10.52 6.294e-12 388-401 PR00048A 10.52 6.824e-12 360-373 PR00048B 6.02 9.308e-11 516-525 PR00048B 6.02 1.563e-10 404-413 PR00048A 10.52 2.174e-10 192-205 PR00048A 10.52 4.522e-10 332-345 PR00048A 10.52 6.087e-10 248-261 PR00048A 10.52 7.261e-10 500-513 PR00048A 10.52 8.043e-10 416-429 PR00048B 6.02 8.313e-10 460-469 PR00048A 10.52 2.440e-09 444-457
1661	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.529e-14 531-547 BL00028 16.07 7.750e-13 195-211 BL00028 16.07 3.348e-12 223-239 BL00028 16.07 2.385e-11 307-323 BL00028 16.07 5.846e-11 447-463 BL00028 16.07 6.538e-11 503-519 BL00028 16.07 7.231e-11 363-379 BL00028 16.07 7.577e-11 419-435 BL00028 16.07 9.308e-11 391-407 BL00028

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Table 3

SEQ ID	Database entry ID	Description	Results*
			16.07 5.800e-10 335-351 BL00028 16.07 6.100e-10 279-295 BL00028 16.07 4.600e-09 251-267
1665	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.857e-30 178-220
1665	BL00032	'Homeobox' antennapedia-type protein.	BL00032C 11.28 2.260e-18 206-223 BL00032B 10.83 1.942e-14 167-205
1665	PR00024	HOMEBOX SIGNATURE	PR00024C 7.49 7.750e-14 210-219 PR00024B 11.27 1.000e-12 200-210
1665	PR00025	HOMEOTIC ANTENNAPEDIA PROTEIN SIGNATURE	PR00025B 11.94 7.000e-11 164-179
1665	PR00031	LAMBDA AND OTHER REPRESSOR HELIX-TURN-HELIX SIGNATURE	PR00031B 16.29 3.172e-10 201-217
1665	PR00026	ENGRAILED HOMEODOMAIN SIGNATURE	PR00026A 7.47 8.714e-10 162-179
1669	PF00992	Troponin.	PF00992A 16.67 5.855e-09 53-87
1671	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.500e-13 479-491 PD00066 13.92 2.714e-12 507-519
1671	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 1.000e-13 460-473 PR00048A 10.52 5.737e-11 516-529 PR00048A 10.52 7.261e-10 488-501 PR00048B 6.02 5.263e-09 476-485
1671	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 3.423e-11 463-479 BL00028 16.07 1.900e-10 491-507 BL00028 16.07 4.600e-10 402-418 BL00028 16.07 4.600e-09 548-564 BL00028 16.07 9.486e-09 434-450
1674	PF00628	PHD-finger.	PF00628 15.84 3.571e-10 325-339
1680	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.500e-16 142-158 BL00028 16.07 8.714e-16 170-186 BL00028 16.07 9.357e-16 282-298 BL00028 16.07 6.063e-15 310-326 BL00028 16.07 5.235e-14 198-214 BL00028 16.07 6.850e-13 226-242 BL00028 16.07 1.783e-12 366-382 BL00028 16.07 3.348e-12 338-354 BL00028 16.07 4.522e-12 254-270 BL00028 16.07 9.609e-12 421-437
1680	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 6.538e-15 326-338 PD00066 13.92 2.800e-14 354-366 PD00066 13.92 2.500e-13 242-254 PD00066 13.92 3.500e-13 382-394 PD00066 13.92 6.500e-13 298-310 PD00066 13.92 8.000e-13 158-170 PD00066 13.92 6.143e-12 186-198 PD00066 13.92 9.571e-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			12 214-226 PD00066 13.92 3.077e-10 409-421 PD00066 13.92 6.192e-10 270-282
1680	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 3.250e-16 307-320 PR00048A 10.52 5.091e-15 139-152 PR00048A 10.52 7.545e-15 195-208 PR00048A 10.52 9.182e-15 335-348 PR00048A 10.52 5.500e-14 167-180 PR00048A 10.52 5.500e-14 251-264 PR00048A 10.52 1.529e-12 223-236 PR00048B 6.02 6.000e-12 295-304 PR00048A 10.52 1.474e-11 363-376 PR00048A 10.52 2.421e-11 279-292 PR00048B 6.02 7.231e-11 239-248 PR00048B 6.02 7.231e-11 379-388 PR00048B 6.02 1.563e-10 211-220 PR00048B 6.02 2.688e-10 351-360 PR00048A 10.52 8.826e-10 418-431 PR00048B 6.02 1.947e-09 434-443 PR00048B 6.02 3.368e-09 323-332
1683	BL00226	Intermediate filaments proteins.	BL00226B 23.86 3.824e-19 76-123 BL00226D 19.10 2.650e-18 225-271
1684	BL00027	'Homeobox' domain proteins.	BL00027 26.43 7.500e-25 101-143
1684	PR00026	ENGRAILED HOMEODOMAIN SIGNATURE	PR00026A 7.47 1.000e-10 85-102
1684	PR00024	HOMEBOX SIGNATURE	PR00024C 7.49 2.038e-10 133-142
1684	BL00032	'Homeobox' antennapedia-type protein.	BL00032C 11.28 7.465e-11 129-146 BL00032B 10.83 9.571e-09 90-128
1689	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 4.780e-17 909-942
1689	PF00856	SET domain proteins.	PF00856B 16.42 5.179e-22 891-912 PF00856A 26.14 6.339e-16 837-873
1689	DM00406	GLIADIN.	DM00406 7.73 8.784e-10 585-597
1689	BL00884	Osteopontin proteins.	BL00884B 12.47 8.853e-10 69-112
1689	BL00422	Granins proteins.	BL00422C 16.18 1.882e-09 176-203
1689	PR00239	MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE	PR00239E 1.58 6.318e-09 586-597
1689	PF00624	Flocculin repeat proteins.	PF00624I 9.10 6.669e-09 39-68
1689	DM00191	w SPAC8A4.04C RESISTANCE SPAC8A4.05C DAUNORUBICIN.	DM00191C 10.57 6.918e-09 44-59
1689	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.	BL00319C 17.12 6.921e-09 65-98
1689	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.813e-12 577-591 PR00049D 0.00 1.500e-10

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Table 3

SEQ ID	Database entry ID	Description	Results*
			582-596 PR00049D 0.00 1.929e-10 581-595 PR00049D 0.00 2.220e-09 579-593 PR00049D 0.00 2.220e-09 580-594 PR00049D 0.00 5.119e-09 321-335 PR00049D 0.00 5.729e-09 578-592 PR00049D 0.00 7.102e-09 585-599 PR00049D 0.00 7.559e-09 583-597 PR00049D 0.00 7.559e-09 584-598
1689	PF00774	Dihydropyridine sensitive L-type calcium channel (Beta subuni.	PF00774A 16.47 5.703e-09 43-88 PF00774A 16.47 8.216e-09 36-81
1689	PD02059	CORE POLYPROTEIN PROTEIN GAG CONTAINS: P.	PD02059B 24.48 8.479e-09 296-330
1689	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 8.941e-11 570-602 DM00215 19.43 5.661e-10 565-597 DM00215 19.43 6.946e-10 321-353 DM00215 19.43 7.107e-10 301-333 DM00215 19.43 1.000e-09 564-596 DM00215 19.43 3.593e-09 318-350 DM00215 19.43 9.542e-09 572-604
1690	PR00179	LIPOCALIN SIGNATURE	PR00179B 9.56 2.071e-09 70-82
1692	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.438e-15 195-211 BL00028 16.07 2.059e-14 335-351 BL00028 16.07 8.412e-14 279-295 BL00028 16.07 4.150e-13 167-183 BL00028 16.07 4.150e-13 307-323 BL00028 16.07 1.000e-12 139-155 BL00028 16.07 2.385e-11 251-267 BL00028 16.07 4.462e-11 111-127 BL00028 16.07 5.200e-10 223-239
1692	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e-16 155-167 PD00066 13.92 8.200e-16 323-335 PD00066 13.92 2.800e-14 183-195 PD00066 13.92 2.286e-12 211-223 PD00066 13.92 4.429e-12 295-307 PD00066 13.92 1.391e-11 267-279 PD00066 13.92 8.435e-11 239-251 PD00066 13.92 5.500e-10 127-139
1692	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 5.500e-17 192-205 PR00048A 10.52 7.000e-17 164-177 PR00048A 10.52 1.818e-15 276-289 PR00048A 10.52 7.000e-14 136-149 PR00048A 10.52 7.750e-14 332-345 PR00048A 10.52 6.786e-13 304-317 PR00048A 10.52 7.353e-12 220-233 PR00048B 6.02 2.385e-11 264-273 PR00048A 10.52 3.368e-11 248-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			261 PR00048A 10.52 4.316e-11 108-121 PR00048B 6.02 8.615e-11 152-161 PR00048B 6.02 2.688e-10 320-329 PR00048B 6.02 6.063e-10 180-189 PR00048B 6.02 9.438e-10 292-301
1692	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970A 8.50 7.750e-09 306-312
1694	BL00970	Nuclear transition protein 2 proteins.	BL00970B 10.09 6.172e-10 357-382 BL00970B 10.09 6.440e-09 355-380
1694	BL00048	Protamine P1 proteins.	BL00048 6.39 5.119e-15 334-360 BL00048 6.39 2.328e-14 332-358 BL00048 6.39 5.985e-13 322-348 BL00048 6.39 1.926e-12 349-375 BL00048 6.39 5.500e-12 328-354 BL00048 6.39 2.625e-11 347-373 BL00048 6.39 2.750e-11 330-356 BL00048 6.39 3.250e-11 363-389 BL00048 6.39 3.375e-11 326-352 BL00048 6.39 4.375e-11 344-370 BL00048 6.39 5.000e-11 357-383 BL00048 6.39 7.000e-11 350-376 BL00048 6.39 7.375e-11 324-350 BL00048 6.39 8.375e-11 369-395 BL00048 6.39 9.000e-11 346-372 BL00048 6.39 9.000e-11 367-393 BL00048 6.39 9.375e-11 335-361 BL00048 6.39 1.355e-10 365-391 BL00048 6.39 1.711e-10 331-357 BL00048 6.39 2.658e-10 361-387 BL00048 6.39 2.895e-10 320-346 BL00048 6.39 2.895e-10 327-353 BL00048 6.39 2.895e-10 336-362 BL00048 6.39 3.013e-10 329-355 BL00048 6.39 4.197e-10 359-385 BL00048 6.39 5.500e-10 337-363 BL00048 6.39 5.974e-10 348-374 BL00048 6.39 6.092e-10 358-384 BL00048 6.39 7.395e-10 333-359 BL00048 6.39 9.171e-10 360-386 BL00048 6.39 9.645e-10 352-378 BL00048 6.39 1.000e-09 356-382 BL00048 6.39 2.800e-09 338-364 BL00048 6.39 3.025e-09 264-290 BL00048 6.39 3.025e-09 321-347 BL00048 6.39 3.700e-09 355-381 BL00048 6.39 3.813e-09 354-380 BL00048 6.39 4.600e-09 351-377 BL00048 6.39 5.838e-09 345-371 BL00048 6.39 7.300e-09 325-351 BL00048 6.39 7.300e-09 366-392 BL00048 6.39 7.638e-09 319-345 BL00048 6.39 7.863e-09 323-349
1694	DM01206	CORONAVIRUS NUCLEOCAPSID	DM01206B 10.69 9.372e-16 367-

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Table 3

SEQ ID	Database entry ID	Description	Results*
		PROTEIN.	386 DM01206B 10.69 4.000e-13 361-380 DM01206B 10.69 7.000e-13 326-345 DM01206B 10.69 9.368e-13 363-382 DM01206B 10.69 4.714e-12 328- 347 DM01206B 10.69 8.429e-12 371-390 DM01206B 10.69 9.857e-12 324-343 DM01206B 10.69 1.672e-11 365-384 DM01206B 10.69 3.687e-11 332- 351 DM01206B 10.69 4.575e-10 330-349 DM01206B 10.69 5.192e-10 359-378 DM01206B 10.69 8.274e-10 357-376 DM01206B 10.69 8.767e-10 320- 339 DM01206B 10.69 3.734e-09 369-388 DM01206B 10.69 4.418e-09 334-353 DM01206B 10.69 9.886e-09 338-357
1696	BL01106	Ribosomal protein L18e proteins.	BL01106B 27.89 5.690e-14 20-74
1697	DM01767	5 TRANSMITTER DOMAIN.	DM01767B 10.07 7.868e-09 164- 180
1699	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 5.355e-23 84- 105
1699	BL00411	Kinesin motor domain proteins.	BL00411C 15.04 8.138e-24 84- 105 BL00411E 10.43 6.023e-13 133-151 BL00411A 11.31 3.930e-09 3-17 BL00411B 13.51 4.405e-09 50-66
1700	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.500e-11 112- 128 BL00028 16.07 2.800e-10 140-156 BL00028 16.07 7.000e- 10 51-67 BL00028 16.07 4.600e- 09 84-100
1700	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 6.400e-09 137- 150
1704	PF00711	Beta defensins.	PF00711 15.76 6.127e-12 37-69
1704	BL00940	Gamma-thionins family proteins.	BL00940B 12.41 1.353e-09 90- 101
1704	PR00858	CRUSTACEAN METALLOTHIONEIN SIGNATURE	PR00858B 5.93 1.479e-09 32-50
1704	DM01724	kw ALLERGEN POLLEN CIM1 HOL-LI.	DM01724 8.14 9.366e-10 4-23 DM01724 8.14 6.803e-09 8-27
1704	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243I 31.77 5.235e-10 34-76 BL00243I 31.77 1.507e-09 37-79 BL00243I 31.77 7.211e-09 46-88
1704	BL00317	WAP-type 'four-disulfide core' domain proteins.	BL00317B 14.58 2.216e-09 40-61 BL00317B 14.58 8.784e-09 3-24
1704	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 4.429e-13 31-76 BL00203 13.94 5.747e-11 24-69 BL00203 13.94 3.489e-10 27-72 BL00203 13.94 1.367e-09 57-102 BL00203 13.94 3.296e-09 32-77 BL00203 13.94 5.224e-09 28-73 BL00203 13.94 5.867e-09 35-80

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Table 3

SEQ ID	Database entry ID	Description	Results*
			BL00203 13.94 8.806e-09 52-97
1704	BL00264	Neurohypophysial hormones proteins.	BL00264 8.98 9.053e-09 71-97
1704	PD00866	GLYCOPROTEIN PROTEIN SPIKE E2 PRECURSOR PEPLIMER.	PD00866L 3.73 1.882e-11 4-13 PD00866L 3.73 7.709e-10 51-60 PD00866L 3.73 9.262e-09 1-10
1705	BL00415	Synapsins proteins.	BL00415N 4.29 2.708e-09 12-55
1705	BL00048	Protamine P1 proteins.	BL00048 6.39 5.950e-09 235-261
1705	PF00992	Troponin.	PF00992A 16.67 6.447e-09 254-288
1705	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 6.975e-11 10-24 PR00049D 0.00 5.729e-09 8-22 PR00049D 0.00 6.034e-09 78-92 PR00049D 0.00 6.339e-09 80-94 PR00049D 0.00 7.407e-09 76-90
1705	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 1.706e-11 3-35 DM00215 19.43 7.589e-10 17-49 DM00215 19.43 6.644e-09 15-47 DM00215 19.43 9.390e-09 10-42
1706	BL00349	CTF/NF-I proteins.	BL00349H 15.70 7.097e-09 49-86
1706	PD01234	PROTEIN NUCLEAR BROMODOMAIN TRANS.	PD01234B 15.53 2.607e-09 2-19 PD01234B 15.53 7.107e-09 68-85 PD01234B 15.53 7.107e-09 132-149
1708	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 4.462e-17 573-621 BL00115Z 3.12 7.813e-16 226-274 BL00115Z 3.12 4.027e-15 372-420 BL00115Z 3.12 4.027e-15 469-517 BL00115Z 3.12 4.436e-15 379-427 BL00115Z 3.12 4.436e-15 476-524 BL00115Z 3.12 5.827e-15 233-281 BL00115Z 3.12 6.645e-15 566-614 BL00115Z 3.12 6.097e-14 331-379 BL00115Z 3.12 6.177e-14 428-476 BL00115Z 3.12 7.133e-14 580-628 BL00115Z 3.12 7.372e-14 254-302 BL00115Z 3.12 8.965e-14 525-573 BL00115Z 3.12 1.543e-13 30-78 BL00115Z 3.12 2.784e-13 393-441 BL00115Z 3.12 2.784e-13 490-538 BL00115Z 3.12 6.897e-13 275-323 BL00115Z 3.12 7.983e-13 37-85 BL00115Z 3.12 1.595e-12 282-330 BL00115Z 3.12 2.190e-12 400-448 BL00115Z 3.12 2.190e-12 497-545 BL00115Z 3.12 2.711e-12 247-295 BL00115Z 3.12 3.975e-12 9-57 BL00115Z 3.12 5.314e-12 587-635 BL00115Z 3.12 5.686e-12 518-566 BL00115Z 3.12 5.835e-12 386-434 BL00115Z 3.12 5.835e-12 483-531 BL00115Z 3.12 5.983e-12 296-344

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Table 3

SEQ ID	Database entry ID	Description	Results*
			BL00115Z 3.12 6.132e-12 23-71 BL00115Z 3.12 6.281e-12 268-316 BL00115Z 3.12 7.099e-12 205-253 BL00115Z 3.12 7.917e-12 219-267 BL00115Z 3.12 8.364e-12 324-372 BL00115Z 3.12 8.438e-12 421-469 BL00115Z 3.12 8.587e-12 240-288 BL00115Z 3.12 1.144e-11 317-365 BL00115Z 3.12 2.152e-11 303-351 BL00115Z 3.12 2.800e-11 261-309 BL00115Z 3.12 3.088e-11 58-106 BL00115Z 3.12 3.880e-11 310-358 BL00115Z 3.12 3.952e-11 407-455 BL00115Z 3.12 4.096e-11 212-260 BL00115Z 3.12 4.600e-11 2-50 BL00115Z 3.12 5.536e-11 504-552 BL00115Z 3.12 6.256e-11 16-64 BL00115Z 3.12 7.048e-11 338-386 BL00115Z 3.12 7.120e-11 435-483 BL00115Z 3.12 7.912e-11 289-337 BL00115Z 3.12 8.848e-11 414-462 BL00115Z 3.12 1.209e-10 532-580 BL00115Z 3.12 1.558e-10 511-559 BL00115Z 3.12 2.465e-10 198-246 BL00115Z 3.12 3.372e-10 132-180 BL00115Z 3.12 3.372e-10 365-413 BL00115Z 3.12 3.372e-10 462-510 BL00115Z 3.12 5.953e-10 44-92 BL00115Z 3.12 6.581e-10 125-173 BL00115Z 3.12 9.442e-10 72-120 BL00115Z 3.12 9.930e-10 79-127 BL00115Z 3.12 3.118e-09 51-99 BL00115Z 3.12 3.978e-09 594-642 BL00115Z 3.12 4.176e-09 559-607 BL00115Z 3.12 4.309e-09 65-113 BL00115Z 3.12 7.022e-09 118-166 BL00115Z 3.12 9.537e-09 86-134
1709	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 3.348e-12 168-184 BL00028 16.07 2.385e-11 364-380 BL00028 16.07 2.731e-11 140-156 BL00028 16.07 2.500e-10 280-296 BL00028 16.07 2.500e-10 336-352 BL00028 16.07 3.700e-10 308-324 BL00028 16.07 4.000e-10 224-240 BL00028 16.07 4.000e-10 252-268 BL00028 16.07 8.500e-10 196-212
1709	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.826e-11 380-392 PD00066 13.92 8.615e-10

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Table 3

SEQ ID	Database entry ID	Description	Results*
			324-336
1709	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 6.478e-10 333-346 PR00048A 10.52 6.478e-10 361-374 PR00048A 10.52 7.652e-10 165-178 PR00048A 10.52 1.000e-09 277-290 PR00048A 10.52 3.880e-09 193-206
1710	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 4.706e-14 196-212 BL00028 16.07 3.348e-12 168-184 BL00028 16.07 2.385e-11 392-408 BL00028 16.07 2.731e-11 140-156 BL00028 16.07 2.500e-10 308-324 BL00028 16.07 2.500e-10 364-380 BL00028 16.07 3.700e-10 336-352 BL00028 16.07 4.000e-10 252-268 BL00028 16.07 4.000e-10 280-296 BL00028 16.07 8.500e-10 224-240
1710	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.826e-11 408-420 PD00066 13.92 2.038e-10 212-224 PD00066 13.92 8.615e-10 352-364
1710	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 2.565e-10 193-206 PR00048A 10.52 6.478e-10 361-374 PR00048A 10.52 6.478e-10 389-402 PR00048A 10.52 6.870e-10 221-234 PR00048A 10.52 7.652e-10 165-178 PR00048A 10.52 1.000e-09 305-318
1711	BL00660	Band 4.1 family domain proteins.	BL00660A 31.50 1.000e-40 13-65 BL00660B 17.33 1.000e-40 99-138 BL00660C 23.36 1.000e-40 186-229 BL00660D 13.60 1.000e-26 240-263 BL00660F 35.24 4.724e-25 555-591 BL00660E 23.41 5.091e-23 269-291
1711	PR00661	ERM FAMILY SIGNATURE	PR00661H 11.24 2.688e-28 588-609 PR00661F 25.17 1.191e-27 284-303 PR00661E 11.38 1.321e-26 209-229 PR00661C 9.53 5.114e-26 113-134 PR00661A 12.48 7.000e-26 17-36 PR00661G 15.01 8.200e-24 566-587 PR00661B 11.79 9.438e-24 69-88 PR00661D 9.08 2.125e-21 159-176
1711	PR00935	BAND 4.1 PROTEIN FAMILY SIGNATURE	PR00935C 11.98 3.769e-24 117-137 PR00935D 10.20 6.400e-17 186-202 PR00935A 10.16 1.947e-14 37-49 PR00935B 10.58 3.032e-13 104-117
1711	PF00992	Troponin.	PF00992A 16.67 6.684e-09 357-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			391
1711	BL00326	Tropomyosins proteins.	BL00326B 7.68 7.887e-09 361-409
1712	BL00660	Band 4.1 family domain proteins.	BL00660B 17.33 1.000e-40 67-106 BL00660C 23.36 1.000e-40 154-197 BL00660D 13.60 1.000e-26 208-231 BL00660F 35.24 4.724e-25 523-559 BL00660E 23.41 5.091e-23 237-259
1712	PR00661	ERM FAMILY SIGNATURE	PR00661H 11.24 2.688e-28 556-577 PR00661F 25.17 1.191e-27 252-271 PR00661E 11.38 1.321e-26 177-197 PR00661C 9.53 5.114e-26 81-102 PR00661G 15.01 8.200e-24 534-555 PR00661B 11.79 9.438e-24 37-56 PR00661D 9.08 2.125e-21 127-144 PR00661A 12.48 2.707e-17 17-36
1712	PR00935	BAND 4.1 PROTEIN FAMILY SIGNATURE	PR00935C 11.98 3.769e-24 85-105 PR00935D 10.20 6.400e-17 154-170 PR00935B 10.58 3.032e-13 72-85
1712	PF00992	Troponin.	PF00992A 16.67 6.684e-09 325-359
1712	BL00326	Tropomyosins proteins.	BL00326B 7.68 7.887e-09 329-377
1713	BL00660	Band 4.1 family domain proteins.	BL00660B 17.33 1.000e-40 116-155 BL00660C 23.36 1.000e-40 203-246 BL00660D 13.60 1.000e-26 257-280 BL00660F 35.24 4.724e-25 572-608 BL00660E 23.41 5.091e-23 286-308 BL00660A 31.50 5.667e-21 30-82
1713	PR00661	ERM FAMILY SIGNATURE	PR00661H 11.24 2.688e-28 605-626 PR00661F 25.17 1.191e-27 301-320 PR00661E 11.38 1.321e-26 226-246 PR00661C 9.53 5.114e-26 130-151 PR00661G 15.01 8.200e-24 583-604 PR00661B 11.79 9.438e-24 86-105 PR00661D 9.08 2.125e-21 176-193 PR00661A 12.48 2.246e-15 17-36
1713	PR00935	BAND 4.1 PROTEIN FAMILY SIGNATURE	PR00935C 11.98 3.769e-24 134-154 PR00935D 10.20 6.400e-17 203-219 PR00935A 10.16 1.947e-14 54-66 PR00935B 10.58 3.032e-13 121-134
1713	PF00992	Troponin.	PF00992A 16.67 6.684e-09 374-408
1713	BL00326	Tropomyosins proteins.	BL00326B 7.68 7.887e-09 378-426
1715	PD00066	PROTEIN ZINC-FINGER METAL-	PD00066 13.92 8.200e-16 323-

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Table 3

SEQ ID	Database entry ID	Description	Results*
		BINDI.	335 PD00066 13.92 8.200e-16 379-391 PD00066 13.92 3.769e-15 407-419 PD00066 13.92 5.846e-15 267-279 PD00066 13.92 2.800e-14 239-251 PD00066 13.92 2.800e-14 295-307 PD00066 13.92 4.000e-14 211-223 PD00066 13.92 8.200e-14 351-363 PD00066 13.92 3.143e-12 463-475 PD00066 13.92 5.696e-11 435-447
1715	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.438e-15 391-407 BL00028 16.07 5.765e-14 223-239 BL00028 16.07 8.650e-13 307-323 BL00028 16.07 8.650e-13 447-463 BL00028 16.07 9.100e-13 251-267 BL00028 16.07 9.100e-13 475-491 BL00028 16.07 1.000e-12 419-435 BL00028 16.07 1.783e-12 363-379 BL00028 16.07 1.000e-10 279-295 BL00028 16.07 2.800e-10 195-211 BL00028 16.07 3.829e-09 335-351
1715	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 4.086e-09 40-78
1715	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.000e-17 388-401 PR00048A 10.52 8.500e-17 220-233 PR00048A 10.52 3.250e-14 444-457 PR00048A 10.52 4.000e-14 472-485 PR00048A 10.52 4.750e-14 248-261 PR00048A 10.52 4.214e-13 304-317 PR00048A 10.52 5.500e-13 332-345 PR00048B 6.02 5.500e-13 264-273 PR00048A 10.52 2.059e-12 416-429 PR00048A 10.52 4.176e-12 192-205 PR00048A 10.52 4.706e-12 360-373 PR00048B 6.02 7.231e-11 236-245 PR00048A 10.52 8.579e-11 276-289 PR00048B 6.02 9.308e-11 320-329 PR00048B 6.02 9.308e-11 376-385 PR00048B 6.02 1.563e-10 460-469 PR00048B 6.02 4.375e-10 292-301 PR00048B 6.02 1.474e-09 404-413 PR00048B 6.02 3.368e-09 348-357 PR00048B 6.02 5.737e-09 208-217
1716	PF00992	Troponin.	PF00992A 16.67 3.789e-10 271-305
1717	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.412e-12 309-322

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Table 3

SEQ ID	Database entry ID	Description	Results*
1717	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 4.522e-11 300-312
1717	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.100e-13 312-328 BL00028 16.07 2.200e-10 284-300
1720	PR00795	RYANODINE RECEPTOR SIGNATURE	PR00795A 9.81 6.420e-09 116-137
1723	PR00528	GLUCOCORTICOID RECEPTOR SIGNATURE	PR00528D 10.72 1.273e-28 275-296 PR00528A 11.88 1.000e-26 26-46 PR00528B 8.99 1.098e-26 76-96 PR00528E 10.00 1.257e-26 322-340 PR00528C 14.75 9.372e-24 109-129
1724	PF00877	NLP/P60 family.	PF00877C 10.03 7.485e-09 210-227
1724	PD02913	PROTEIN LARGE TEGUMENT PROBABLE CAPSID ASSEMBLY V.	PD02913G 15.63 8.791e-09 182-203
1725	BL00726	AP endonucleases family 1 proteins.	BL00726D 17.67 8.043e-36 185-218 BL00726E 15.26 4.130e-29 246-271 BL00726C 19.90 8.286e-25 109-134 BL00726F 18.15 6.143e-23 278-300 BL00726B 14.22 7.375e-15 71-81
1728	BL00038	Myc-type, 'helix-loop-helix' dimerization domain proteins.	BL00038A 13.61 5.875e-11 53-68
1728	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 5.146e-11 396-410 PR00456E 3.06 5.146e-11 397-411 PR00456E 3.06 9.250e-10 394-408 PR00456E 3.06 9.250e-10 395-409 PR00456E 3.06 1.000e-09 398-412
1728	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 8.405e-10 396-410 PR00308A 5.90 8.405e-10 397-411 PR00308C 3.83 8.892e-10 396-405 PR00308C 3.83 8.892e-10 397-406 PR00308C 3.83 8.892e-10 398-407 PR00308C 3.83 8.892e-10 399-408 PR00308C 3.83 8.892e-10 400-409 PR00308C 3.83 8.892e-10 401-410 PR00308C 3.83 8.892e-10 402-411 PR00308A 5.90 1.635e-09 395-409 PR00308A 5.90 4.388e-09 393-407 PR00308A 5.90 5.024e-09 398-412
1728	PR00833	POLLEN ALLERGEN POA PI SIGNATURE	PR00833H 2.30 3.192e-09 396-410 PR00833H 2.30 3.192e-09 397-411 PR00833H 2.30 5.500e-09 394-408
1731	PR00116	ARGINASE SIGNATURE	PR00116D 14.91 8.565e-18 271-300
1731	BL00147	Arginase family proteins.	BL00147E 15.08 1.000e-24 270-300 BL00147A 20.22 6.927e-13 76-99 BL00147C 9.48 7.577e-12 158-169 BL00147D 15.27

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Table 3

SEQ ID	Database entry ID	Description	Results*
			7.453e-10 181-203 BL00147F 10.93 1.000e-08 313-323
1732	BL00074	Glu / Leu / Phe / Val dehydrogenases proteins.	BL00074A 25.39 1.000e-40 79-133 BL00074D 20.39 8.875e-28 233-267 BL00074C 14.14 4.130e-21 187-207 BL00074B 10.31 7.429e-17 146-161
1732	PR00082	GLUTAMATE/LEUCINE/PHENYLALANINE/VALINE DEHYDROGENASE SIGNATURE	PR00082B 17.59 1.000e-21 186-208 PR00082C 16.34 1.321e-16 236-256 PR00082A 11.37 2.929e-15 101-115
1734	DM00784	APILLOMAVIRUS E4 PROTEIN.	DM00784A 16.65 7.818e-09 341-365
1734	PR00452	SH3 DOMAIN SIGNATURE	PR00452D 17.02 1.000e-08 616-628
1737	BL00246	Wnt-1 family proteins.	BL00246E 20.32 6.442e-29 251-296 BL00246B 13.69 5.026e-26 48-82 BL00246D 23.97 1.000e-24 128-180 BL00246A 15.75 8.364e-15 15-34 BL00246C 15.56 1.964e-13 93-117
1738	BL00246	Wnt-1 family proteins.	BL00246E 20.32 6.442e-29 355-400 BL00246B 13.69 5.026e-26 152-186 BL00246D 23.97 1.000e-24 232-284 BL00246A 15.75 8.364e-15 119-138 BL00246C 15.56 1.964e-13 197-221
1742	PF00855	PWWP domain proteins.	PF00855 13.75 3.588e-09 148-164
1743	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 5.810e-15 242-275
1744	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 3.880e-09 85-97
1744	PR00501	KELCH REPEAT SIGNATURE	PR00501A 8.25 7.545e-09 420-433
1746	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 1.391e-10 142-155 PR00019B 11.36 1.360e-09 391-404 PR00019A 11.19 1.000e-08 370-383
1747	BL00298	Heat shock hsp90 proteins family proteins.	BL00298E 27.30 8.244e-11 658-712
1747	BL00422	Granins proteins.	BL00422C 16.18 4.000e-09 648-675
1747	DM00552	GROWTH FACTOR AND CYTOKINES RECEPTORS FAMILY.	DM00552D 15.26 7.949e-09 22-45
1747	PF00992	Troponin.	PF00992A 16.67 5.263e-09 643-677 PF00992A 16.67 8.697e-09 636-670
1747	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 2.500e-12 629-679 BL00412D 16.54 8.728e-10 626-676 BL00412D 16.54 1.000e-09 636-686 BL00412D 16.54 9.633e-09 638-688
1747	PF01140	Matrix protein (MA), p15.	PF01140D 15.54 9.686e-09 647-681

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Table 3

SEQ ID	Database entry ID	Description	Results*
1752	BL00826	MARCKS family proteins.	BL00826C 7.63 4.938e-09 125-151
1760	BL00048	Protamine P1 proteins.	BL00048 6.39 8.412e-12 66-92 BL00048 6.39 9.500e-11 68-94 BL00048 6.39 3.013e-10 67-93 BL00048 6.39 6.329e-10 63-89 BL00048 6.39 2.575e-09 61-87 BL00048 6.39 5.613e-09 69-95 BL00048 6.39 6.288e-09 62-88 BL00048 6.39 8.088e-09 60-86 BL00048 6.39 9.663e-09 77-103
1761	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 7.221e-09 50-98
1764	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306B 5.57 1.000e-08 718-728 PD00306B 5.57 1.000e-08 1081-1091
1770	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 4.051e-09 115-129 PR00049D 0.00 5.271e-09 116-130 PR00049D 0.00 5.271e-09 118-132 PR00049D 0.00 5.271e-09 119-133
1770	BL01113	C1q domain proteins.	BL01113A 17.99 2.862e-16 116-142 BL01113A 17.99 6.351e-13 110-136 BL01113A 17.99 8.297e-13 31-57 BL01113A 17.99 8.385e-12 113-139 BL01113A 17.99 1.614e-11 25-51 BL01113A 17.99 1.383e-10 119-145 BL01113A 17.99 4.808e-09 122-148 BL01113A 17.99 7.058e-09 107-133 BL01113A 17.99 8.615e-09 58-84 BL01113A 17.99 8.615e-09 61-87
1770	BL00420	Speract receptor repeat proteins domain proteins.	BL00420A 20.42 2.309e-11 67-95 BL00420A 20.42 5.091e-11 25-53 BL00420A 20.42 6.754e-10 22-50 BL00420A 20.42 8.377e-10 110-138 BL00420A 20.42 6.123e-09 52-80 BL00420A 20.42 6.400e-09 46-74 BL00420A 20.42 6.400e-09 49-77 BL00420A 20.42 9.169e-09 70-98
1775	DM01551	kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER.	DM01551C 14.62 3.400e-09 92-111
1775	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 4.667e-09 27-40 PR00019B 11.36 7.480e-09 70-83
1777	PD00302	PROTEASE POLYPROTEIN HYDROLASE ASP.	PD00302B 9.52 7.120e-14 329-344 PD00302A 6.33 5.935e-11 266-276
1777	PF00692	dUTPase.	PF00692B 8.14 3.613e-11 181-191 PF00692C 11.65 4.162e-09 205-214
1777	BL00141	Eukaryotic and viral aspartyl proteases proteins.	BL00141A 12.10 9.600e-09 263-278
1777	DM00892	3 RETROVIRAL PROTEINASE.	DM00892B 9.78 1.000e-08 332-337

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Table 3

SEQ ID	Database entry ID	Description	Results*
1778	BL00027	'Homeobox' domain proteins.	BL00027 26.43 2.500e-34 200-242
1778	BL00032	'Homeobox' antennapedia-type protein.	BL00032B 10.83 1.164e-29 189-227 BL00032C 11.28 7.750e-20 228-245
1778	PR00031	LAMBDA AND OTHER REPRESSOR HELIX-TURN-HELIX SIGNATURE	PR00031B 16.29 7.652e-12 223-239
1778	PR00025	HOMEOTIC ANTENNAPEDIA PROTEIN SIGNATURE	PR00025B 11.94 3.438e-11 186-201
1778	PR00024	HOMEBOX SIGNATURE	PR00024B 11.27 5.846e-13 222-232 PR00024C 7.49 6.143e-13 232-241 PR00024A 11.87 8.000e-10 207-218
1781	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354B 14.71 7.889e-10 21-48
1786	BL00434	HSF-type DNA-binding domain proteins.	BL00434C 23.85 8.222e-09 399-438
1788	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.217e-20 88-130
1790	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 7.261e-10 89-102
1791	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 2.787e-09 343-391
1792	PF00658	Poly-adenylate binding protein, unique domain proteins.	PF00658B 28.57 1.439e-30 319-365 PF00658A 19.88 5.500e-28 140-179
1792	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 1.600e-10 288-297 BL00030A 14.39 9.500e-10 353-371 BL00030A 14.39 2.714e-09 70-88 BL00030B 7.03 9.526e-09 195-204
1793	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 5.000e-17 69-81
1799	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.017e-11 132-146
1800	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 5.424e-09 521-535
1801	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 3.647e-14 379-395 BL00028 16.07 7.882e-14 239-255 BL00028 16.07 1.900e-13 351-367 BL00028 16.07 6.400e-13 323-339 BL00028 16.07 4.130e-12 267-283 BL00028 16.07 5.304e-12 295-311 BL00028 16.07 7.577e-11 211-227
1801	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.545e-15 376-389 PR00048A 10.52 4.750e-14 320-333 PR00048A 10.52 7.750e-14 292-305 PR00048A 10.52 2.929e-13 236-249 PR00048A 10.52 3.571e-13 348-361 PR00048B 6.02 6.000e-12 252-261 PR00048A 10.52 6.824e-12 208-221 PR00048B 6.02 1.000e-11 280-289

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Table 3

SEQ ID	Database entry ID	Description	Results*
			PR00048A 10.52 2.174e-10 264-277 PR00048B 6.02 4.375e-10 364-373 PR00048B 6.02 5.500e-10 224-233 PR00048B 6.02 7.188e-10 308-317 PR00048B 6.02 7.188e-10 336-345
1801	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 4.462e-15 255-267 PD00066 13.92 5.846e-15 311-323 PD00066 13.92 9.308e-15 367-379 PD00066 13.92 2.800e-14 227-239 PD00066 13.92 2.800e-14 283-295 PD00066 13.92 3.348e-11 339-351 PD00066 13.92 1.000e-09 199-211
1807	BL00478	LIM domain proteins.	BL00478B 14.79 8.826e-14 25-39
1807	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002A 14.19 4.462e-11 173-191 BL50002B 15.18 6.500e-09 211-224
1808	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 5.500e-21 184-214
1808	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 9.294e-12 184-202
1808	BL00239	Receptor tyrosine kinase class II proteins.	BL00239B 25.15 2.935e-09 119-166
1808	BL00240	Receptor tyrosine kinase class III proteins.	BL00240E 11.56 1.000e-08 170-207
1811	BL00380	Rhodanese proteins.	BL00380D 15.90 8.200e-28 130-155 BL00380G 11.26 5.800e-16 287-299 BL00380B 14.77 7.000e-14 69-81 BL00380F 9.76 5.886e-13 223-233 BL00380C 15.67 7.387e-13 102-117 BL00380E 12.44 7.000e-11 201-212 BL00380A 10.48 1.000e-09 30-39
1815	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.000e-13 170-182 PD00066 13.92 7.429e-12 114-126 PD00066 13.92 3.348e-11 142-154
1815	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 9.357e-13 151-164 PR00048A 10.52 3.118e-12 123-136 PR00048A 10.52 5.263e-11 95-108
1815	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 4.913e-12 98-114 BL00028 16.07 7.261e-12 126-142 BL00028 16.07 4.900e-10 154-170
1818	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 9.000e-13 270-282 PD00066 13.92 2.714e-12 158-170 PD00066 13.92 4.000e-12 382-394 PD00066 13.92 1.000e-11 214-226 PD00066 13.92 2.174e-11 186-198 PD00066 13.92 3.739e-11 326-338 PD00066 13.92 6.478e-11

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Table 3

SEQ ID	Database entry ID	Description	Results*
			298-310 PD00066 13.92 8.043e-11 242-254 PD00066 13.92 8.435e-11 562-574 PD00066 13.92 8.826e-11 102-114 PD00066 13.92 6.700e-09 130-142
1818	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 8.941e-14 226-242 BL00028 16.07 3.423e-11 114-130 BL00028 16.07 6.192e-11 338-354 BL00028 16.07 8.269e-11 366-382 BL00028 16.07 8.615e-11 546-562 BL00028 16.07 8.962e-11 574-590 BL00028 16.07 3.100e-10 394-410 BL00028 16.07 3.700e-10 282-298 BL00028 16.07 5.500e-10 254-270 BL00028 16.07 7.000e-10 310-326 BL00028 16.07 7.900e-10 518-534 BL00028 16.07 3.314e-09 198-214 BL00028 16.07 4.600e-09 142-158 BL00028 16.07 6.400e-09 86-102 BL00028 16.07 7.943e-09 170-186
1818	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 2.286e-13 223-236 PR00048A 10.52 6.786e-13 111-124 PR00048A 10.52 6.294e-12 543-556 PR00048A 10.52 4.316e-11 363-376 PR00048A 10.52 6.684e-11 167-180 PR00048A 10.52 8.105e-11 251-264 PR00048A 10.52 3.739e-10 307-320 PR00048A 10.52 6.870e-10 391-404 PR00048A 10.52 7.652e-10 335-348 PR00048B 6.02 8.875e-10 323-332 PR00048A 10.52 2.800e-09 83-96 PR00048B 6.02 4.316e-09 379-388 PR00048B 6.02 6.684e-09 155-164 PR00048A 10.52 7.840e-09 571-584 PR00048B 6.02 9.053e-09 211-220 PR00048B 6.02 1.000e-08 559-568
1821	PR00625	DNAJ PROTEIN FAMILY SIGNATURE	PR00625B 13.48 5.632e-10 59-79 PR00625A 12.84 6.910e-10 26-45
1821	BL00636	Nt-dnaJ domain proteins.	BL00636B 15.11 9.455e-11 59-79 BL00636A 8.07 1.000e-09 30-46
1824	BL00904	Protein prenyltransferases alpha subunit repeat proteins proteins.	BL00904A 8.30 4.667e-10 60-109
1824	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 6.667e-10 62-74
1824	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.000e-13 487-499 PD00066 13.92 7.857e-12 242-254 PD00066 13.92 3.348e-11 287-299 PD00066 13.92

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Table 3

SEQ ID	Database entry ID	Description	Results*
			3.348e-11 606-618 PD00066 13.92 5.846e-10 515-527 PD00066 13.92 7.923e-10 785- 797 PD00066 13.92 3.700e-09 813-825 PD00066 13.92 3.700e- 09 869-881
1824	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479A 19.86 4.064e-09 514-536
1824	PR00608	CLASS II CYTOCHROME C SIGNATURE	PR00608A 13.74 4.158e-09 678-701
1824	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 5.235e-11 60-74 PR00049D 0.00 4.814e-09 62-76
1824	PR00239	MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE	PR00239E 1.58 5.398e-09 64-75 PR00239E 1.58 5.500e-09 69-80
1824	BL00415	Synapsins proteins.	BL00415N 4.29 6.912e-09 59-102
1824	PF00624	Flocculin repeat proteins.	PF00624I 9.10 2.984e-09 89-118 PF00624I 9.10 7.307e-09 88-117
1824	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 4.150e-13 226-242 BL00028 16.07 9.550e-13 299-315 BL00028 16.07 9.550e-13 499-515 BL00028 16.07 8.435e-12 471-487 BL00028 16.07 4.462e-11 853-869 BL00028 16.07 5.846e-11 328-344 BL00028 16.07 7.577e-11 797-813 BL00028 16.07 4.600e-10 527-543 BL00028 16.07 5.500e-10 910-926 BL00028 16.07 6.100e-10 362-378 BL00028 16.07 7.300e-10 825-841 BL00028 16.07 3.057e-09 769-785 BL00028 16.07 3.057e-09 938-954 BL00028 16.07 8.200e-09 254-270 BL00028 16.07 8.714e-09 618-634
1824	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 9.085e-09 43-75
1824	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.412e-12 496-509 PR00048B 6.02 6.538e-11 484-493 PR00048A 10.52 4.913e-10 524-537 PR00048A 10.52 5.304e-10 296-309 PR00048A 10.52 8.826e-10 223-236 PR00048A 10.52 4.960e-09 822-835 PR00048A 10.52 6.760e-09 794-807 PR00048A 10.52 9.280e-09 251-264 PR00048B 6.02 9.526e-09 810-819
1825	BL00326	Tropomyosins proteins.	BL00326C 9.99 7.174e-09 239-292
1830	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.800e-14 138-150 PD00066 13.92 2.800e-14 278-290 PD00066 13.92 7.000e-13 250-262 PD00066 13.92 1.000e-12 166-178 PD00066 13.92 5.286e-12 222-234

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Table 3

SEQ ID	Database entry ID	Description	Results*
			PD00066 13.92 7.429e-12 194-206
1830	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.438e-15 122-138 BL00028 16.07 2.957e-12 150-166 BL00028 16.07 5.304e-12 84-100 BL00028 16.07 1.692e-11 206-222 BL00028 16.07 4.115e-11 178-194 BL00028 16.07 6.538e-11 290-306 BL00028 16.07 8.269e-11 262-278 BL00028 16.07 1.000e-10 234-250
1830	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479A 19.86 9.561e-10 193-215
1830	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 2.500e-14 231-244 PR00048A 10.52 1.000e-13 147-160 PR00048A 10.52 8.714e-13 119-132 PR00048A 10.52 8.714e-13 287-300 PR00048A 10.52 5.235e-12 175-188 PR00048A 10.52 1.947e-11 259-272 PR00048A 10.52 3.842e-11 81-94 PR00048A 10.52 5.737e-11 203-216 PR00048B 6.02 5.846e-11 275-284 PR00048B 6.02 5.500e-10 135-144 PR00048B 6.02 7.750e-10 163-172 PR00048B 6.02 7.158e-09 219-228 PR00048B 6.02 8.105e-09 191-200 PR00048B 6.02 9.526e-09 303-312
1831	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE	PR00300A 9.56 5.563e-10 10-28
1831	BL00674	AAA-protein family proteins.	BL00674B 4.46 4.162e-09 7-28
1834	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.286e-12 269-281
1834	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.217e-12 253-269 BL00028 16.07 1.346e-11 281-297
1834	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.714e-13 278-291 PR00048B 6.02 5.263e-09 266-275 PR00048B 6.02 5.263e-09 294-303 PR00048A 10.52 9.280e-09 250-263
1838	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 6.815e-10 60-69 PR00308C 3.83 8.892e-10 57-66 PR00308C 3.83 8.892e-10 58-67 PR00308C 3.83 8.714e-09 56-65
1849	BL00478	LIM domain proteins.	BL00478B 14.79 3.000e-11 93-107
1852	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 9.667e-09 42-50
1854	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926F 17.75 1.522e-09 28-50

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Table 3

SEQ ID	Database entry ID	Description	Results*
1854	PR00927	ADENINE NUCLEOTIDE TRANSLOCATOR 1 SIGNATURE	PR00927B 14.66 2.397e-13 189-210 PR00927B 14.66 3.959e-09 287-308
1854	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 9.625e-17 26-50 BL00215A 15.82 2.532e-11 252-276 BL00215B 10.44 4.000e-09 199-211 BL00215B 10.44 4.900e-09 297-309
1854	PR00784	MITOCHONDRIAL BROWN FAT UNCOUPLING PROTEIN SIGNATURE	PR00784D 15.86 5.061e-09 199-216 PR00784D 15.86 7.915e-09 297-314
1856	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301A 10.24 1.900e-09 310-320
1856	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.300e-16 650-662 PD00066 13.92 5.846e-15 678-690 PD00066 13.92 8.435e-11 594-606 PD00066 13.92 2.500e-09 566-578
1856	BL00354	HMG-I and HMG-Y DNA-binding domain proteins (A+T-hook).	BL00354C 6.61 6.178e-09 331-345
1856	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 4.029e-10 743-763 PR00211B 0.86 5.583e-09 749-769 PR00211B 0.86 6.833e-09 737-757
1856	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 8.533e-10 327-377 BL00412D 16.54 2.102e-09 328-378 BL00412D 16.54 6.051e-09 325-375 BL00412D 16.54 6.602e-09 285-335 BL00412D 16.54 7.429e-09 314-364 BL00412D 16.54 8.255e-09 280-330
1856	BL00795	Involucrin proteins.	BL00795C 17.06 8.400e-09 342-386
1856	PF00922	Vesiculovirus phosphoprotein.	PF00922A 19.17 8.448e-09 305-338
1856	PR00930	HIGH MOBILITY GROUP PROTEIN (HMGY) SIGNATURE	PR00930E 5.98 8.500e-09 332-344
1856	BL00422	Granins proteins.	BL00422C 16.18 8.235e-09 352-379 BL00422C 16.18 8.941e-09 299-326
1856	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 4.130e-12 662-678 BL00028 16.07 9.217e-12 578-594 BL00028 16.07 8.615e-11 690-706 BL00028 16.07 4.300e-10 520-536 BL00028 16.07 1.514e-09 550-566 BL00028 16.07 3.571e-09 466-482 BL00028 16.07 9.229e-09 493-509
1856	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 9.640e-09 58-70
1856	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 3.571e-13 575-588 PR00048A 10.52 5.235e-12 659-672 PR00048A 10.52

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Table 3

SEQ ID	Database entry ID	Description	Results*
			2.440e-09 687-700 PR00048A 10.52 9.640e-09 517-530
1856	PR00047	C4-TYPE STEROID RECEPTOR ZINC FINGER SIGNATURE	PR00047B 7.63 1.000e-08 577-592
1857	PF01140	Matrix protein (MA), p15.	PF01140D 15.54 7.240e-11 230-264
1857	PF00992	Troponin.	PF00992A 16.67 2.050e-13 219-253 PF00992A 16.67 1.355e-09 234-268
1857	BL00224	Clathrin light chain proteins.	BL00224B 16.94 5.909e-09 250-302
1859	PD01966	TRANSFERASE GLYCOSYLTRANSFERASE.	PD01966E 31.30 9.710e-18 359-410 PD01966D 19.10 5.080e-15 243-283
1860	PD02807	APOLIPOPROTEIN E PRECURSOR APO-E GLYCOPROTEIN PLAS.	PD02807D 7.99 5.809e-09 353-402
1861	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 7.261e-10 89-102
1863	BL00021	Kringle domain proteins.	BL00021D 24.56 8.036e-21 205-246 BL00021B 13.33 5.071e-18 46-63
1863	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE	PR00722A 12.27 6.040e-15 47-62 PR00722C 10.87 5.500e-11 195-207
1863	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134A 11.96 5.500e-16 46-62 BL00134C 13.45 6.400e-15 233-246 BL00134B 15.99 6.268e-11 196-219
1863	BL00495	Apple domain proteins.	BL00495O 13.75 4.740e-16 224-252 BL00495K 12.58 6.300e-12 48-80 BL00495M 8.50 5.631e-10 116-150 BL00495N 11.04 6.676e-09 188-222
1863	BL01253	Type I fibronectin domain proteins.	BL01253H 13.15 4.136e-25 215-249 BL01253G 11.34 2.658e-12 195-208 BL01253D 4.84 9.862e-11 46-59 BL01253F 14.35 9.621e-10 151-189 BL01253E 16.01 6.753e-09 114-150
1865	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 8.071e-10 227-259
1865	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 7.317e-10 237-257 PR00211B 0.86 5.417e-09 231-251
1869	PD02059	CORE POLYPROTEIN PROTEIN GAG CONTAINS: P.	PD02059B 24.48 5.364e-10 46-80
1869	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.500e-14 26-40 PR00049D 0.00 6.250e-12 30-44 PR00049D 0.00 7.277e-11 32-46 PR00049D 0.00 7.580e-11 28-42 PR00049D 0.00 8.109e-11 27-41 PR00049D 0.00 8.185e-11 29-43 PR00049D 0.00 9.714e-10 53-67 PR00049D 0.00 9.786e-10 33-47 PR00049D 0.00 3.136e-09 31-45

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Table 3

SEQ ID	Database entry ID	Description	Results*
1869	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 8.875e-12 43-75 DM00215 19.43 1.176e-11 33-65 DM00215 19.43 4.529e-11 49-81 DM00215 19.43 6.464e-10 44-76 DM00215 19.43 8.393e-10 30-62 DM00215 19.43 1.000e-09 34-66 DM00215 19.43 3.593e-09 29-61 DM00215 19.43 3.746e-09 31-63 DM00215 19.43 4.966e-09 32-64 DM00215 19.43 5.271e-09 39-71
1869	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 8.917e-09 57-77
1871	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 8.200e-09 499-512
1871	DM00315	072 RIBONUCLEASE INHIBITOR.	DM00315G 15.85 8.740e-09 520-555
1872	BL00632	Ribosomal protein S4 proteins.	BL00632 23.79 1.189e-10 92-134
1874	PR00315	GTP-BINDING ELONGATION FACTOR SIGNATURE	PR00315A 11.81 3.093e-11 9-22
1874	BL00301	GTP-binding elongation factors proteins.	BL00301B 20.09 3.625e-15 91-122 BL00301A 12.41 3.613e-11 9-20
1874	BL01176	Initiation factor 2 proteins.	BL01176B 8.74 7.520e-11 88-125
1874	PR00318	ALPHA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00318E 7.23 1.000e-08 141-150
1875	BL00301	GTP-binding elongation factors proteins.	BL00301B 20.09 4.960e-24 91-122 BL00301A 12.41 6.625e-12 21-32
1875	PR00315	GTP-BINDING ELONGATION FACTOR SIGNATURE	PR00315A 11.81 1.000e-14 21-34 PR00315C 13.85 8.875e-12 89-99
1875	BL01176	Initiation factor 2 proteins.	BL01176B 8.74 4.490e-11 88-125
1876	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 9.586e-10 785-830
1876	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE	PR00300A 9.56 7.429e-09 325-343
1876	BL00936	Ribosomal protein L35 proteins.	BL00936A 11.46 7.568e-09 884-902
1880	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 5.200e-30 9-47
1881	PR00209	ALPHA/BETA GLIADIN FAMILY SIGNATURE	PR00209B 4.88 4.563e-09 59-77
1883	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.500e-28 195-237
1883	BL00035	'POU' domain proteins.	BL00035C 17.40 7.845e-12 202-231
1883	BL00478	LIM domain proteins.	BL00478B 14.79 1.000e-16 85-99 BL00478B 14.79 8.500e-12 25-39
1883	PR00024	HOMEBOX SIGNATURE	PR00024C 7.49 4.682e-11 227-236
1883	PR00031	LAMBDA AND OTHER REPRESSOR HELIX-TURN-HELIX SIGNATURE	PR00031B 16.29 8.560e-11 218-234
1883	BL00032	'Homeobox' antennapedia-type protein.	BL00032C 11.28 3.554e-10 223-240
1885	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.800e-14 249-261 PD00066 13.92 2.500e-13 404-416

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Table 3

SEQ ID	Database entry ID	Description	Results*
1885	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048B 6.02 7.750e-10 401-410 PR00048A 10.52 8.043e-10 413-426 PR00048B 6.02 8.313e-10 246-255 PR00048A 10.52 2.800e-09 258-271
1885	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.217e-12 388-404 BL00028 16.07 1.600e-10 233-249 BL00028 16.07 4.343e-09 159-175
1888	BL00027	'Homeobox' domain proteins.	BL00027 26.43 3.700e-23 216-258
1888	PR00031	LAMBDA AND OTHER REPRESSOR HELIX-TURN-HELIX SIGNATURE	PR00031B 16.29 4.240e-11 239-255
1888	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 6.813e-10 47-61 PR00456E 3.06 1.797e-09 45-59
1888	PR00024	HOMEODOMAIN SIGNATURE	PR00024C 7.49 7.900e-09 248-257
1890	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 5.404e-29 26-64
1890	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 5.500e-13 591-604 PR00048A 10.52 2.588e-12 445-458 PR00048A 10.52 3.118e-12 473-486 PR00048A 10.52 6.294e-12 249-262 PR00048A 10.52 6.294e-12 305-318 PR00048A 10.52 6.824e-12 535-548 PR00048A 10.52 7.353e-12 417-430 PR00048A 10.52 7.353e-12 563-576 PR00048A 10.52 7.353e-12 619-632 PR00048A 10.52 3.842e-11 277-290 PR00048A 10.52 5.737e-11 361-374 PR00048B 6.02 8.615e-11 579-588 PR00048B 6.02 2.125e-10 635-644 PR00048A 10.52 3.348e-10 647-660 PR00048A 10.52 4.522e-10 389-402 PR00048B 6.02 5.500e-10 321-330 PR00048B 6.02 6.625e-10 607-616 PR00048B 6.02 7.188e-10 551-560 PR00048A 10.52 8.826e-10 193-206 PR00048A 10.52 8.826e-10 703-716 PR00048A 10.52 9.609e-10 507-520 PR00048B 6.02 1.000e-09 265-274 PR00048A 10.52 4.240e-09 221-234 PR00048B 6.02 4.789e-09 461-470
1890	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.077e-15 240-252 PD00066 13.92 3.077e-15 268-280 PD00066 13.92 3.077e-15 554-566 PD00066 13.92 3.077e-15 582-594 PD00066 13.92 3.077e-15 638-650 PD00066 13.92 7.231e-15 526-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			538 PD00066 13.92 4.600e-14 296-308 PD00066 13.92 5.800e-14 408-420 PD00066 13.92 6.000e-13 324-336 PD00066 13.92 8.500e-13 722-734 PD00066 13.92 9.000e-13 464-476 PD00066 13.92 9.000e-13 610-622 PD00066 13.92 1.000e-12 666-678 PD00066 13.92 1.692e-10 436-448 PD00066 13.92 1.300e-09 380-392 PD00066 13.92 2.200e-09 352-364 PD00066 13.92 4.900e-09 498-510
1890	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 4.706e-14 448-464 BL00028 16.07 1.450e-13 566-582 BL00028 16.07 5.500e-13 594-610 BL00028 16.07 9.100e-13 622-638 BL00028 16.07 4.130e-12 308-324 BL00028 16.07 4.913e-12 280-296 BL00028 16.07 4.913e-12 420-436 BL00028 16.07 6.885e-11 252-268 BL00028 16.07 6.885e-11 706-722 BL00028 16.07 8.962e-11 476-492 BL00028 16.07 1.900e-10 224-240 BL00028 16.07 1.000e-09 392-408 BL00028 16.07 2.800e-09 538-554 BL00028 16.07 2.800e-09 650-666 BL00028 16.07 3.829e-09 196-212 BL00028 16.07 6.657e-09 364-380
1891	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 3.250e-15 12-50
1893	PD02625	DECARBOXYLASE BIOSYNTHESIS S-ADENOSYLMETHIONINE.	PD02625A 10.33 8.500e-10 274-285
1894	PD02625	DECARBOXYLASE BIOSYNTHESIS S-ADENOSYLMETHIONINE.	PD02625A 10.33 8.500e-10 339-350
1895	BL00813	Eukaryotic initiation factor 4E proteins.	BL00813B 24.44 3.864e-32 91-134 BL00813D 23.58 7.353e-30 169-212 BL00813C 14.40 8.435e-18 152-167 BL00813A 15.06 7.088e-16 62-79
1898	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 4.375e-15 298-314 BL00028 16.07 1.000e-14 382-398 BL00028 16.07 4.706e-14 354-370 BL00028 16.07 3.700e-13 466-482 BL00028 16.07 4.150e-13 326-342 BL00028 16.07 5.500e-11 438-454 BL00028 16.07 7.923e-11 410-426
1898	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.800e-14 342-354 PD00066 13.92 2.800e-14

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Table 3

SEQ ID	Database entry ID	Description	Results*
			398-410 PD00066 13.92 2.800e-14 454-466 PD00066 13.92 8.800e-14 370-382 PD00066 13.92 9.400e-14 426-438 PD00066 13.92 4.913e-11 314-326 PD00066 13.92 1.000e-09 286-298
1898	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 1.000e-15 295-308 PR00048A 10.52 3.455e-15 463-476 PR00048A 10.52 9.182e-15 351-364 PR00048A 10.52 1.750e-14 323-336 PR00048A 10.52 4.214e-13 379-392 PR00048A 10.52 7.353e-12 435-448 PR00048B 6.02 1.000e-11 339-348 PR00048B 6.02 1.000e-11 395-404 PR00048B 6.02 6.538e-11 367-376 PR00048A 10.52 1.783e-10 407-420 PR00048B 6.02 2.688e-10 451-460 PR00048B 6.02 1.947e-09 423-432
1899	BL00031	Nuclear hormones receptors DNA-binding region proteins.	BL00031A 19.55 6.318e-22 280-312
1899	PR00398	STEROID HORMONE RECEPTOR SIGNATURE	PR00398A 14.44 1.726e-15 280-297
1899	PR00047	C4-TYPE STEROID RECEPTOR ZINC FINGER SIGNATURE	PR00047A 15.70 8.650e-18 280-296 PR00047B 7.63 8.448e-10 296-311
1899	PR00350	VITAMIN D RECEPTOR SIGNATURE	PR00350A 10.48 7.968e-09 280-296
1899	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306B 5.57 8.500e-09 101-111
1899	DM00191	w SPAC8A4.04C RESISTANCE SPAC8A4.05C DAUNORUBICIN.	DM00191A 8.16 9.160e-09 94-106
1903	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111E 17.28 7.253e-10 48-96
1909	BL01098	Lipolytic enzymes G-D-S-L family, serine proteins.	BL01098B 14.98 7.840e-09 195-205
1913	BL00027	'Homeobox' domain proteins.	BL00027 26.43 3.700e-23 306-348
1913	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 7.888e-09 412-462
1917	BL00411	Kinesin motor domain proteins.	BL00411H 15.66 8.541e-22 176-206 BL00411G 21.39 2.841e-21 126-167 BL00411E 10.43 4.343e-15 19-37 BL00411F 14.77 5.350e-12 78-102
1917	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380D 9.93 5.109e-16 177-198 PR00380C 13.18 1.706e-11 125-143 PR00380B 12.64 5.500e-10 87-104
1918	BL00031	Nuclear hormones receptors DNA-binding region proteins.	BL00031A 19.55 5.680e-30 153-185
1918	PR00047	C4-TYPE STEROID RECEPTOR ZINC	PR00047A 15.70 3.250e-18 153-

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Table 3

SEQ ID	Database entry ID	Description	Results*
		FINGER SIGNATURE	169 PR00047B 7.63 9.719e-16 169-184
1918	PR00398	STEROID HORMONE RECEPTOR SIGNATURE	PR00398A 14.44 4.086e-23 153-170 PR00398B 15.08 9.419e-12 174-190
1918	PR00350	VITAMIN D RECEPTOR SIGNATURE	PR00350A 10.48 3.202e-10 153-169
1919	BL00674	AAA-protein family proteins.	BL00674A 16.91 5.696e-09 1-21
1921	PF00075	RNase H.	PF00075F 12.87 2.588e-10 94-104
1924	BL00053	Ribosomal protein S8 proteins.	BL00053C 16.71 5.219e-24 98-130 BL00053B 14.56 8.500e-11 58-75
1926	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.059e-27 10-48
1926	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 8.313e-15 242-258 BL00028 16.07 4.706e-14 382-398 BL00028 16.07 1.783e-12 354-370 BL00028 16.07 6.087e-12 270-286 BL00028 16.07 3.077e-11 214-230 BL00028 16.07 6.192e-11 326-342 BL00028 16.07 2.200e-10 186-202 BL00028 16.07 8.800e-10 298-314
1926	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 5.500e-17 379-392 PR00048A 10.52 5.909e-15 351-364 PR00048A 10.52 3.250e-14 267-280 PR00048A 10.52 8.500e-14 239-252 PR00048A 10.52 6.824e-12 323-336 PR00048B 6.02 1.000e-11 227-236 PR00048B 6.02 1.692e-11 283-292 PR00048A 10.52 6.211e-11 183-196 PR00048A 10.52 6.684e-11 211-224 PR00048B 6.02 6.063e-10 367-376 PR00048B 6.02 6.625e-10 339-348 PR00048B 6.02 9.438e-10 199-208 PR00048B 6.02 3.842e-09 311-320 PR00048A 10.52 4.960e-09 295-308
1926	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e-17 342-354 PD00066 13.92 8.200e-14 202-214 PD00066 13.92 8.800e-14 370-382 PD00066 13.92 5.500e-13 286-298 PD00066 13.92 7.000e-13 230-242 PD00066 13.92 6.087e-11 258-270 PD00066 13.92 5.200e-09 314-326
1927	BL00226	Intermediate filaments proteins.	BL00226D 19.10 5.935e-33 378-424 BL00226B 23.86 4.375e-20 211-258 BL00226C 13.23 3.195e-14 277-307 BL00226A 12.77 3.543e-10 110-124
1928	PD01066	PROTEIN ZINC FINGER ZINC-FINGER	PD01066 19.43 4.566e-26 41-79

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Table 3

SEQ ID	Database entry ID	Description	Results*
		METAL-BINDING NU.	
1928	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 6.850e-13 396-412 BL00028 16.07 8.650e-13 480-496 BL00028 16.07 4.462e-11 508-524 BL00028 16.07 9.308e-11 284-300 BL00028 16.07 5.800e-10 424-440 BL00028 16.07 7.300e-10 452-468 BL00028 16.07 8.800e-10 312-328 BL00028 16.07 1.000e-09 340-356 BL00028 16.07 2.029e-09 368-384
1928	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 1.600e-14 356-368 PD00066 13.92 2.800e-14 328-340 PD00066 13.92 2.800e-14 412-424 PD00066 13.92 2.800e-14 496-508 PD00066 13.92 1.000e-13 468-480 PD00066 13.92 6.500e-13 384-396 PD00066 13.92 2.714e-12 524-536 PD00066 13.92 3.143e-12 440-452 PD00066 13.92 9.100e-09 300-312
1928	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048B 6.02 6.400e-13 409-418 PR00048A 10.52 6.786e-13 477-490 PR00048A 10.52 5.235e-12 505-518 PR00048B 6.02 9.000e-12 381-390 PR00048A 10.52 2.895e-11 393-406 PR00048B 6.02 5.846e-11 325-334 PR00048B 6.02 5.846e-11 493-502 PR00048B 6.02 2.688e-10 353-362 PR00048A 10.52 4.913e-10 365-378 PR00048A 10.52 5.304e-10 449-462 PR00048B 6.02 8.313e-10 437-446 PR00048B 6.02 1.474e-09 465-474 PR00048B 6.02 3.368e-09 297-306 PR00048A 10.52 4.600e-09 421-434 PR00048A 10.52 8.560e-09 533-546 PR00048A 10.52 8.920e-09 337-350 PR00048A 10.52 9.640e-09 281-294
1929	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 8.875e-37 10-48
1929	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.000e-13 488-504 BL00028 16.07 8.200e-13 432-448 BL00028 16.07 2.174e-12 236-252 BL00028 16.07 2.174e-12 600-616 BL00028 16.07 2.565e-12 628-644 BL00028 16.07 3.739e-12 180-196 BL00028 16.07 3.739e-12 208-224 BL00028 16.07 4.130e-12 320-336 BL00028 16.07

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Table 3

SEQ ID	Database entry ID	Description	Results*
			5.696e-12 264-280 BL00028 16.07 5.696e-12 572-588 BL00028 16.07 7.652e-12 516-532 BL00028 16.07 7.652e-12 656-672 BL00028 16.07 8.043e-12 348-364 BL00028 16.07 9.217e-12 460-476 BL00028 16.07 9.609e-12 544-560 BL00028 16.07 1.346e-11 376-392 BL00028 16.07 4.115e-11 292-308 BL00028 16.07 2.200e-10 404-420
1929	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 1.600e-14 196-208 PD00066 13.92 2.800e-14 252-264 PD00066 13.92 2.800e-14 560-572 PD00066 13.92 5.200e-14 308-320 PD00066 13.92 5.200e-14 364-376 PD00066 13.92 1.500e-13 420-432 PD00066 13.92 1.500e-13 616-628 PD00066 13.92 3.000e-13 224-236 PD00066 13.92 3.000e-13 280-292 PD00066 13.92 3.000e-13 588-600 PD00066 13.92 6.000e-13 448-460 PD00066 13.92 1.857e-12 644-656 PD00066 13.92 4.429e-12 504-516 PD00066 13.92 7.857e-12 532-544 PD00066 13.92 6.087e-11 476-488 PD00066 13.92 6.870e-11 392-404 PD00066 13.92 1.000e-09 336-348
1929	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479A 19.86 5.404e-09 503-525
1929	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 9.182e-15 233-246 PR00048A 10.52 4.000e-14 485-498 PR00048A 10.52 6.250e-14 289-302 PR00048A 10.52 2.929e-13 597-610 PR00048A 10.52 5.500e-13 373-386 PR00048A 10.52 6.143e-13 317-330 PR00048A 10.52 1.000e-12 345-358 PR00048A 10.52 3.118e-12 457-470 PR00048A 10.52 3.647e-12 653-666 PR00048A 10.52 4.176e-12 513-526 PR00048A 10.52 4.176e-12 569-582 PR00048A 10.52 6.294e-12 625-638 PR00048A 10.52 7.353e-12 177-190 PR00048A 10.52 7.882e-12 429-442 PR00048A 10.52 8.941e-12 261-274 PR00048A 10.52 8.941e-12 541-554 PR00048A 10.52 3.842e-11 205-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			218 PR00048B 6.02 9.308e-11 361-370 PR00048B 6.02 4.375e-10 193-202 PR00048B 6.02 4.375e-10 501-510 PR00048B 6.02 6.063e-10 249-258 PR00048B 6.02 7.188e-10 557-566 PR00048B 6.02 8.875e-10 389-398 PR00048B 6.02 9.438e-10 305-314 PR00048B 6.02 1.947e-09 277-286 PR00048B 6.02 2.895e-09 669-678 PR00048B 6.02 5.263e-09 417-426 PR00048B 6.02 5.263e-09 613-622 PR00048B 6.02 5.737e-09 333-342 PR00048B 6.02 7.158e-09 221-230 PR00048B 6.02 7.632e-09 585-594 PR00048B 6.02 1.000e-08 445-454
1930	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 3.302e-31 15-53 PD01066 19.43 9.800e-30 112-150
1930	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970A 8.50 3.700e-09 573-579
1930	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.000e-14 394-406 PD00066 13.92 2.500e-13 562-574 PD00066 13.92 3.000e-13 506-518 PD00066 13.92 9.000e-13 730-742 PD00066 13.92 9.500e-13 758-770 PD00066 13.92 9.571e-12 590-602 PD00066 13.92 3.739e-11 646-658 PD00066 13.92 8.826e-11 366-378 PD00066 13.92 3.400e-09 618-630 PD00066 13.92 6.700e-09 534-546
1930	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 3.348e-12 574-590 BL00028 16.07 4.913e-12 602-618 BL00028 16.07 9.217e-12 714-730 BL00028 16.07 5.500e-11 742-758 BL00028 16.07 7.923e-11 406-422 BL00028 16.07 9.308e-11 350-366 BL00028 16.07 2.200e-10 658-674 BL00028 16.07 2.800e-10 546-562 BL00028 16.07 4.300e-10 518-534 BL00028 16.07 6.700e-10 490-506 BL00028 16.07 1.771e-09 770-786 BL00028 16.07 3.571e-09 630-646 BL00028 16.07 6.143e-09 434-450 BL00028 16.07 8.200e-09 378-394
1930	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.364e-15 739-752 PR00048A 10.52 4.706e-12 711-724 PR00048A 10.52

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Table 3

SEQ ID	Database entry ID	Description	Results*
			6.294e-12 599-612 PR00048A 10.52 7.882e-12 403-416 PR00048A 10.52 6.684e-11 375-388 PR00048A 10.52 8.579e-11 767-780 PR00048A 10.52 1.391e-10 571-584 PR00048A 10.52 4.130e-10 347-360 PR00048A 10.52 4.130e-10 655-668 PR00048A 10.52 8.043e-10 515-528 PR00048B 6.02 8.313e-10 615-624 PR00048A 10.52 8.826e-10 627-640 PR00048B 6.02 2.895e-09 503-512 PR00048B 6.02 2.895e-09 727-736 PR00048B 6.02 3.842e-09 643-652 PR00048B 6.02 4.316e-09 559-568 PR00048B 6.02 4.789e-09 531-540 PR00048A 10.52 8.560e-09 487-500 PR00048B 6.02 9.526e-09 587-596
1932	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 6.684e-11 176-189 PR00048A 10.52 1.000e-10 62-75 PR00048A 10.52 1.000e-10 90-103 PR00048A 10.52 4.522e-10 146-159 PR00048A 10.52 1.360e-09 118-131
1932	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.200e-09 109-121
1932	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.731e-11 65-81 BL00028 16.07 1.900e-10 93-109 BL00028 16.07 4.600e-10 149-165 BL00028 16.07 5.200e-10 179-195 BL00028 16.07 5.800e-10 121-137 BL00028 16.07 7.686e-09 215-231
1933	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 6.864e-20 172-210
1933	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 4.938e-15 622-638 BL00028 16.07 2.059e-14 594-610 BL00028 16.07 6.294e-14 426-442 BL00028 16.07 1.900e-13 510-526 BL00028 16.07 3.250e-13 734-750 BL00028 16.07 4.150e-13 454-470 BL00028 16.07 5.500e-13 538-554 BL00028 16.07 9.100e-13 566-582 BL00028 16.07 1.000e-11 482-498 BL00028 16.07 3.077e-11 398-414 BL00028 16.07 5.154e-11 650-666 BL00028 16.07 5.846e-11 678-694 BL00028 16.07 1.600e-10 706-722 BL00028 16.07 5.629e-09 370-386
1933	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 9.182e-15 619-

426
Table 3

SEQ ID	Database entry ID	Description	Results*
			632 PR00048A 10.52 1.000e-14 423-436 PR00048A 10.52 1.000e-14 507-520 PR00048A 10.52 8.500e-14 479-492 PR00048A 10.52 6.143e-13 675- 688 PR00048A 10.52 1.000e-12 731-744 PR00048A 10.52 6.294e-12 591-604 PR00048B 6.02 1.000e-11 663-672 PR00048A 10.52 4.789e-11 451- 464 PR00048A 10.52 4.789e-11 703-716 PR00048B 6.02 5.154e- 11 691-700 PR00048B 6.02 5.846e-11 467-476 PR00048B 6.02 7.231e-11 719-728 PR00048A 10.52 9.053e-11 647- 660 PR00048B 6.02 9.308e-11 439-448 PR00048A 10.52 1.000e-10 535-548 PR00048B 6.02 2.125e-10 607-616 PR00048B 6.02 3.250e-10 551- 560 PR00048B 6.02 3.250e-10 747-756 PR00048A 10.52 6.478e-10 563-576 PR00048B 6.02 6.625e-10 635-644 PR00048B 6.02 1.474e-09 411- 420 PR00048B 6.02 3.368e-09 495-504 PR00048A 10.52 3.520e-09 395-408 PR00048A 10.52 4.600e-09 367-380 PR00048B 6.02 6.211e-09 523- 532 PR00048B 6.02 7.158e-09 579-588
1933	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e-16 470- 482 PD00066 13.92 6.538e-15 498-510 PD00066 13.92 1.600e- 14 722-734 PD00066 13.92 2.800e-14 442-454 PD00066 13.92 2.800e-14 666-678 PD00066 13.92 4.600e-14 610- 622 PD00066 13.92 4.600e-14 694-706 PD00066 13.92 5.000e- 13 414-426 PD00066 13.92 9.500e-13 526-538 PD00066 13.92 6.870e-11 582-594 PD00066 13.92 4.462e-10 638- 650 PD00066 13.92 5.154e-10 358-370 PD00066 13.92 7.231e- 10 386-398 PD00066 13.92 7.600e-09 554-566
1933	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970A 8.50 7.750e-09 733- 739
1936	BL00038	Myc-type, 'helix-loop-helix' dimerization domain proteins.	BL00038B 16.97 1.273e-11 98- 118 BL00038A 13.61 4.375e-11 75-90
1937	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.929e-16 332-

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Table 3

SEQ ID	Database entry ID	Description	Results*
			348 BL00028 16.07 8.714e-16 668-684 BL00028 16.07 6.824e-14 220-236 BL00028 16.07 7.353e-14 696-712 BL00028 16.07 8.941e-14 360-376 BL00028 16.07 5.500e-13 276-292 BL00028 16.07 1.391e-12 192-208 BL00028 16.07 3.348e-12 612-628 BL00028 16.07 4.130e-12 500-516 BL00028 16.07 4.522e-12 304-320 BL00028 16.07 8.043e-12 556-572 BL00028 16.07 1.000e-11 388-404 BL00028 16.07 1.000e-11 416-432 BL00028 16.07 4.115e-11 584-600 BL00028 16.07 8.269e-11 752-768 BL00028 16.07 1.300e-10 724-740 BL00028 16.07 1.600e-10 472-488 BL00028 16.07 3.100e-10 248-264 BL00028 16.07 3.400e-10 444-460 BL00028 16.07 7.300e-10 528-544 BL00028 16.07 4.857e-09 640-656
1937	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.545e-15 665-678 PR00048A 10.52 2.500e-14 329-342 PR00048A 10.52 5.500e-14 553-566 PR00048A 10.52 8.500e-14 217-230 PR00048A 10.52 9.250e-14 497-510 PR00048A 10.52 2.929e-13 273-286 PR00048A 10.52 2.929e-13 301-314 PR00048A 10.52 4.214e-13 693-706 PR00048A 10.52 5.500e-13 609-622 PR00048A 10.52 5.500e-13 749-762 PR00048A 10.52 6.143e-13 413-426 PR00048A 10.52 4.176e-12 357-370 PR00048B 6.02 8.000e-12 625-634 PR00048A 10.52 5.737e-11 385-398 PR00048A 10.52 9.526e-11 189-202 PR00048A 10.52 9.526e-11 525-538 PR00048A 10.52 1.783e-10 721-734 PR00048B 6.02 3.250e-10 289-298 PR00048B 6.02 3.250e-10 429-438 PR00048B 6.02 3.813e-10 485-494 PR00048A 10.52 4.522e-10 581-594 PR00048A 10.52 5.696e-10 469-482 PR00048B 6.02 8.313e-10 513-522 PR00048B 6.02 8.313e-10 709-718 PR00048B 6.02 8.313e-10 737-746 PR00048A

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Table 3

SEQ ID	Database entry ID	Description	Results*
			10.52 9.609e-10 637-650 PR00048B 6.02 1.000e-09 457-466 PR00048B 6.02 2.895e-09 541-550 PR00048B 6.02 3.842e-09 569-578 PR00048B 6.02 7.158e-09 261-270 PR00048A 10.52 7.840e-09 245-258 PR00048B 6.02 9.053e-09 597-606
1937	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.231e-15 600-612 PD00066 13.92 2.800e-14 292-304 PD00066 13.92 2.800e-14 488-500 PD00066 13.92 2.800e-14 628-640 PD00066 13.92 5.200e-14 544-556 PD00066 13.92 3.000e-13 572-584 PD00066 13.92 3.500e-13 264-276 PD00066 13.92 6.000e-13 208-220 PD00066 13.92 3.143e-12 740-752 PD00066 13.92 3.739e-11 656-668 PD00066 13.92 5.304e-11 320-332 PD00066 13.92 5.304e-11 348-360 PD00066 13.92 5.846e-10 684-696 PD00066 13.92 8.962e-10 516-528 PD00066 13.92 2.200e-09 460-472 PD00066 13.92 3.400e-09 712-724 PD00066 13.92 8.500e-09 376-388 PD00066 13.92 8.500e-09 432-444 PD00066 13.92 9.400e-09 236-248
1938	PF00084	Sushi domain proteins (SCR repeat proteins).	PF00084B 9.45 9.100e-09 283-294
1939	PF00084	Sushi domain proteins (SCR repeat proteins).	PF00084B 9.45 9.100e-09 132-143
1941	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 4.667e-09 2086-2094
1941	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 8.806e-09 2263-2313
1942	BL00632	Ribosomal protein S4 proteins.	BL00632 23.79 4.000e-38 87-129
1942	BL01280	Glucose inhibited division protein A family proteins.	BL01280H 19.43 5.545e-11 42-88

*Results include in order: accession number subtype; raw score; p-value; position of signature in amino acid sequence.

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Table 4A

SEQ ID	Model	Description	E-value	Score
972	globin	Globin	2.9e-45	162.3
973	arginase	Arginase family	8.8e-159	540.9
974	arginase	Arginase family	5.9e-155	528.2
975	arginase	Arginase family	4.5e-167	568.5
979	PID	Phosphotyrosine interaction domain (PTB/PID).	1.2e-102	354.4
980	PID	Phosphotyrosine interaction domain (PTB/PID).	1.2e-102	354.4
981	zf-C4	Zinc finger, C4 type (two domains)	2.9e-42	144.8
983	Exonuclease	Exonuclease	4.9e-21	83.3
986	ank	Ank repeat	2.5e-39	144.1
987	zf-C2H2	Zinc finger, C2H2 type	2.7e-119	409.7
989	CUB	CUB domain	2.8e-20	80.8
990	FKBP	FKBP-type peptidyl-prolyl cis-trans isomerase	3e-35	119.1
992	cpn60_TCP1	TCP-1/cpn60 chaperonin family	7.3e-154	524.5
994	WD40	WD domain, G-beta repeat	5.2e-21	83.2
995	LIM_bind	LIM-domain binding protein	6.3e-287	966.6
997	UCH-2	Ubiquitin carboxyl-terminal hydrolase family 2	9.8e-26	98.9
998	Transposase_22	L1 transposable element	3e-06	-69.2
999	FAD_binding_4	FAD binding domain	1.3e-66	234.7
1007	myb_DNA-binding	Myb-like DNA-binding domain	6e-10	40.5
1008	proteasome	Proteasome A-type and B-type	6.9e-51	182.5
1011	DnaJ	DnaJ domain	4.7e-16	66.8
1012	Fe_hyd_lg_C	Iron only hydrogenase large subunit, C-terminal domain	6e-156	531.5
1014	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	1.5e-20	81.7
1015	TPR	TPR Domain	1.8e-18	74.8
1018	tubulin	Tubulin/FtsZ family	3.1e-280	944.4
1019	tRNA-synt_2	tRNA synthetases class II (D, K and N)	1.1e-169	577.1
1022	abhydrolase	alpha/beta hydrolase fold	4.5e-20	80.1
1025	zf-C2H2	Zinc finger, C2H2 type	4e-73	256.3
1029	ParBc	ParB-like nuclease domain	0.033	7.3
1030	Pribosyltran	Phosphoribosyl transferase domain	5.4e-17	69.9
1032	ig	Immunoglobulin domain	5.3e-08	30.8
1033	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	3.8e-41	150.1
1034	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.1e-15	55.1
1035	Worm_family_8	Putative membrane protein	6.2e-58	205.9
1037	HSP20	Hsp20/alpha crystallin family	1.2e-10	43.2
1039	LRR	Leucine Rich Repeat	1.9e-09	44.8
1040	LRR	Leucine Rich Repeat	1.9e-09	44.8
1041	Ribosomal_L28e	Ribosomal L28e protein family	1.4e-65	231.3
1042	FKBP	FKBP-type peptidyl-prolyl cis-trans isomerase	1.5e-23	80.8
1043	GST_C	Glutathione S-transferase, C-terminal domain	1.2e-31	116.3
1044	GST_N	Glutathione S-transferase, N-terminal domain	1.3e-26	97.2
1045	GST_N	Glutathione S-transferase, N-terminal domain	1.3e-26	97.2

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Table 4A

SEQ ID	Model	Description	E-value	Score
1047	adh_zinc	Zinc-binding dehydrogenases	2.3e-91	317.0
1054	SAICAR_synt	SAICAR synthetase	6.5e-111	381.9
1061	zf-C2H2	Zinc finger, C2H2 type	4.2e-159	542.0
1064	zf-C2H2	Zinc finger, C2H2 type	9.4e-160	544.1
1069	Myosin_tail	Myosin tail	6.8e-17	67.8
1074	pkinase	Protein kinase domain	9.9e-52	185.3
1076	zf-C2H2	Zinc finger, C2H2 type	3.3e-13	57.3
1077	zf-C2H2	Zinc finger, C2H2 type	8.7e-11	49.3
1084	NUDIX	MutT-like domain	0.0018	23.5
1089	zf-C2H2	Zinc finger, C2H2 type	3.7e-189	641.8
1090	PX	PX domain	3.1e-16	67.4
1093	cyclin	Cyclin, N-terminal domain	9.7e-46	165.4
1095	A1pp	Appr-1"-p processing enzyme family	7.9e-39	142.4
1096	60s_ribosomal	60s Acidic ribosomal protein	1.6e-34	112.9
1103	C2	C2 domain	3.6e-21	83.8
1105	CAP_GLY	CAP-Gly domain	3.4e-26	100.4
1106	Band_41	FERM domain (Band 4.1 family)	1.4e-114	358.4
1107	Band_41	FERM domain (Band 4.1 family)	1.4e-114	358.4
1110	WD40	WD domain, G-beta repeat	7.2e-08	39.6
1114	IQ	IQ calmodulin-binding motif	0.011	22.4
1115	zf-C2H2	Zinc finger, C2H2 type	1.3e-76	267.9
1116	Kelch	Kelch motif	4.1e-38	140.0
1117	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	2.3e-05	21.7
1118	zf-C2H2	Zinc finger, C2H2 type	2.4e-29	110.9
1119	Band_7	SPFH domain / Band 7 family	2e-30	114.5
1122	zf-C2H2	Zinc finger, C2H2 type	3.7e-107	369.4
1124	tRNA-synt_1c	tRNA synthetases class I (E and Q)	1.5e-118	407.2
1126	UCH-2	Ubiquitin carboxyl-terminal hydrolase family 2	6.9e-21	82.8
1128	PAX	'Paired box' domain	1.7e-88	307.4
1132	SH3	SH3 domain	0.0025	14.3
1136	DUF71	Domain of unknown function DUF71	6.8e-83	288.8
1137	SCP	SCP-like extracellular protein	2.2e-10	41.2
1139	Ribosomal_L44	Ribosomal protein L44	7.5e-41	149.1
1141	RCC1	Regulator of chromosome condensation (RCC1)	4.3e-09	37.0
1144	RUN	RUN domain	0.00018	24.8
1148	ank	Ank repeat	1.4e-29	111.8
1149	chromo	'chromo' (CHRromatin Organization MODifier) domain	1.7e-24	88.4
1153	CH	Calponin homology (CH) domain	2.4e-29	110.9
1156	efhand	EF hand	7.4e-20	79.4
1159	DSPc	Dual specificity phosphatase, catalytic domain	0.00019	0.9
1161	zf-C2H2	Zinc finger, C2H2 type	1.6e-30	114.9
1162	C1q	C1q domain	5.3e-09	39.0
1164	kinesin	Kinesin motor domain	6e-115	395.3
1165	C2	C2 domain	0.087	5.3
1168	UBX	UBX domain	0.013	15.3
1169	KRAB	KRAB box	4.5e-32	120.0
1172	zf-C2H2	Zinc finger, C2H2 type	8.2e-59	208.8
1173	NUDIX	MutT-like domain	0.0078	16.8
1174	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.6
1176	zf-C2H2	Zinc finger, C2H2 type	6.6e-07	36.4

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Table 4A

SEQ ID	Model	Description	E-value	Score
1179	EMP24_GP25L	emp24/gp25L/p24 family	0.06	-40.8
1180	RhoGEF	RhoGEF domain	9.5e-15	62.4
1181	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0012	16.1
1184	actin	Actin	2.4e-09	32.0
1185	ig	Immunoglobulin domain	1.4e-45	152.0
1186	FYVE	FYVE zinc finger	1.8e-19	74.1
1188	globin	Globin	2.4e-38	138.2
1190	Adenylsucc_synt	Adenylosuccinate synthetase	0	1075.1
1191	Rhodanese	Rhodanese-like domain	3.9e-07	37.1
1193	adh_zinc	Zinc-binding dehydrogenases	1.4e-77	271.2
1202	F-box	F-box domain	1.5e-05	31.9
1204	zf-C2H2	Zinc finger, C2H2 type	6.3e-34	126.1
1205	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.6e-15	52.8
1212	zf-C2H2	Zinc finger, C2H2 type	2.2e-24	94.5
1213	COX6B	Cytochrome oxidase c subunit VIb	1.9e-58	207.6
1214	Sec7	Sec7 domain	3e-104	359.8
1219	ZZ	Zinc finger present in dystrophin, CBP/p300	6.7e-10	46.3
1220	zf-CXXC	CXXC zinc finger	1.2e-15	65.4
1224	HMG_box	HMG (high mobility group) box	6.2e-18	73.0
1225	zf-C2H2	Zinc finger, C2H2 type	1.4e-75	264.5
1226	Kelch	Kelch motif	6.2e-09	43.1
1227	Kelch	Kelch motif	8.9e-11	49.2
1228	DENN	DENN (AEX-3) domain	7e-30	111.1
1229	zf-C2H2	Zinc finger, C2H2 type	2.1e-59	210.8
1230	Nebulin_repeat	Nebulin repeat	1.7e-62	221.0
1231	TPR	TPR Domain	1.4e-05	32.0
1235	BRCT	BRCA1 C Terminus (BRCT) domain	1.1e-09	35.9
1236	zf-B_box	B-box zinc finger.	1.4e-07	38.6
1238	mito_carr	Mitochondrial carrier protein	1.9e-74	260.8
1239	Armadillo_seg	Armadillo/beta-catenin-like repeat	3.2e-07	37.4
1240	mbt	mbt repeat	1.5e-123	423.9
1243	BTB	BTB/POZ domain	1.3e-17	72.0
1245	TruB_N	TruB family pseudouridylate synthase (N terminal domain)	5.8e-45	162.8
1247	zf-C2H2	Zinc finger, C2H2 type	2.6e-98	340.0
1248	helicase_C	Helicase conserved C-terminal domain	1.2e-22	88.6
1249	MAGE	MAGE family	1.4e-15	65.2
1253	C2	C2 domain	1.9e-27	104.6
1254	C2	C2 domain	1.4e-32	121.7
1255	KH-domain	KH domain	5.1e-42	153.0
1256	ig	Immunoglobulin domain	4.4e-10	37.5
1261	SH2	SH2 domain	8e-26	78.1
1263	TPR	TPR Domain	4.2e-05	30.4
1267	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	3.7e-11	40.5
1272	UBX	UBX domain	3.2e-29	110.5
1273	GTF2I	GTF2I-like repeat	3.4e-41	150.3
1277	BTB	BTB/POZ domain	5.4e-23	89.8
1278	zf-C2H2	Zinc finger, C2H2 type	3.8e-59	209.9
1282	PHD	PHD-finger	7.3e-14	59.5
1285	UCH-2	Ubiquitin carboxyl-terminal	2.2e-18	74.5

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Table 4A

SEQ ID	Model	Description	E-value	Score
		hydrolase family 2		
1287	PP2C	Protein phosphatase 2C	3.4e-25	92.1
1288	PP2C	Protein phosphatase 2C	1.9e-24	89.5
1294	BPL_LipA_LipB	Biotin/lipoate A/B protein ligase family	3.5e-22	87.1
1295	crystall	Beta/Gamma crystallin	8.4e-95	328.4
1299	ank	Ank repeat	2.8e-42	153.9
1301	fn3	Fibronectin type III domain	3.7e-07	37.2
1302	K_tetra	K ⁺ channel tetramerisation domain	6.2e-09	43.1
1307	zf-MYND	MYND finger	2.5e-09	44.4
1311	Ribosomal_L24e	Ribosomal protein L24e	5.4e-50	179.5
1314	WD40	WD domain, G-beta repeat	1.9e-18	74.7
1315	Aldose_epim	Aldose 1-epimerase	2.2e-106	366.8
1319	zf-C2H2	Zinc finger, C2H2 type	4.1e-92	319.4
1324	Ribosomal_S10	Ribosomal protein S10p/S20e	5.5e-32	119.7
1325	homeobox	Homeobox domain	3.5e-58	206.7
1327	ank	Ank repeat	1.3e-21	85.2
1330	zf-C2H2	Zinc finger, C2H2 type	6.6e-91	315.4
1331	SCAN	SCAN domain	1.3e-57	204.8
1332	MyTH4	MyTH4 domain	1.4e-19	78.5
1333	LRRCT	Leucine rich repeat C-terminal domain	5.9e-10	46.5
1337	DnaJ	DnaJ domain	1.8e-18	74.8
1344	zf-C2H2	Zinc finger, C2H2 type	1.6e-71	251.0
1349	zf-C2H2	Zinc finger, C2H2 type	2.2e-50	180.8
1350	rvp	Retroviral aspartyl protease	0.015	14.2
1351	SH3	SH3 domain	3.1e-17	70.7
1352	adenylatekinase	Adenylate kinase	7.9e-66	232.1
1354	COX6B	Cytochrome oxidase c subunit VIb	1.9e-32	120.7
1356	Ribosomal_L37e	Ribosomal protein L37e	3.2e-31	117.1
1358	Troponin	Troponin	9.2e-35	128.9
1360	Glyco_transf_10	Glycosyltransferase family 10 (fucosyltransferase)	2.5e-07	-22.5
1361	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	6.3e-09	33.2
1362	rvt	Reverse transcriptase (RNA-dependent DNA polymerase)	3.1e-29	110.6
1364	KRAB	KRAB box	4e-37	136.8
1367	zf-C2H2	Zinc finger, C2H2 type	1.5e-126	433.8
1370	bromodomain	Bromodomain	1.2e-30	110.3
1371	Peptidase_M1	Peptidase family M1	3.6e-116	337.0
1372	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	1.8e-21	84.8
1376	zf-C2H2	Zinc finger, C2H2 type	1.2e-111	384.3
1380	Mtap_PNP	Phosphorylase family 2	2e-159	543.0
1386	zf-C2H2	Zinc finger, C2H2 type	1.5e-18	75.0
1387	F-box	F-box domain	0.00019	28.2
1389	zf-C2H2	Zinc finger, C2H2 type	1.1e-117	404.4
1391	kinesin	Kinesin motor domain	2.7e-79	276.9
1394	Mov34	Mov34/MPN/PAD-1 family	6.2e-28	106.2
1395	T-box	T-box	1.8e-128	440.2
1397	zf-C2H2	Zinc finger, C2H2 type	9.6e-114	391.3
1398	WD40	WD domain, G-beta repeat	9.9e-23	88.9
1400	Dynein_heavy	Dynein heavy chain	4.5e-233	787.7
1401	Ribosomal_L11	Ribosomal protein L11	6.2e-53	189.3

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Table 4A

SEQ ID	Model	Description	E-value	Score
1403	PWWP	PWWP domain	1.1e-10	49.0
1404	zf-C2H2	Zinc finger, C2H2 type	1e-205	696.8
1408	FYVE	FYVE zinc finger	4.7e-28	104.5
1415	FYVE	FYVE zinc finger	1.4e-12	49.6
1417	CH	Calponin homology (CH) domain	5.7e-16	66.5
1418	PH	PH domain	2.3e-21	81.0
1419	PH	PH domain	2.3e-21	81.0
1420	pkinase	Protein kinase domain	7e-24	90.0
1423	PA28_beta	Proteasome activator pa28 beta subunit	1.9e-114	393.6
1425	thioredo	Thioredoxin	0.0096	13.5
1427	K_tetra	K ⁺ channel tetramerisation domain	2.4e-15	64.4
1430	ank	Ank repeat	2.4e-63	223.9
1431	HLH	Helix-loop-helix DNA-binding domain	2.6e-11	51.0
1434	zf-C2H2	Zinc finger, C2H2 type	8.1e-191	647.3
1437	Ribosomal_L29	Ribosomal L29 protein	1.3e-14	62.0
1439	zf-C2H2	Zinc finger, C2H2 type	6e-88	305.6
1440	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	0.099	13.2
1446	zf-C2H2	Zinc finger, C2H2 type	2e-100	347.0
1451	zf-C2H2	Zinc finger, C2H2 type	5.3e-115	395.5
1454	zf-C2H2	Zinc finger, C2H2 type	1.7e-157	536.6
1455	zf-C2H2	Zinc finger, C2H2 type	1.8e-37	137.9
1457	SCAN	SCAN domain	5.6e-61	216.0
1458	pKID	pKID domain	4.6e-24	93.4
1459	LRR	Leucine Rich Repeat	0.00013	28.8
1460	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	0.0011	25.7
1462	ABC1	ABC1 family	1.3e-41	151.7
1463	Pur_DNA_glyco	Methylpurine-DNA glycosylase (MPG)	6.5e-118	405.1
1464	Pur_DNA_glyco	Methylpurine-DNA glycosylase (MPG)	1.7e-120	413.7
1465	Troponin	Troponin	2e-19	78.0
1466	CUB	CUB domain	5.5e-83	289.1
1470	trypsin	Trypsin	2.4e-32	104.6
1471	trypsin	Trypsin	6.7e-91	288.8
1478	zf-C2H2	Zinc finger, C2H2 type	2.4e-26	100.9
1480	zf-C2H2	Zinc finger, C2H2 type	1.5e-29	111.6
1488	zf-C2H2	Zinc finger, C2H2 type	2.5e-23	90.9
1489	Ets	Ets-domain	6.9e-36	131.4
1493	TTL	Tubulin-tyrosine ligase family	2.6e-15	64.3
1496	DnaJ	DnaJ domain	4.7e-40	146.5
1497	homeobox	Homeobox domain	9.5e-22	85.7
1501	homeobox	Homeobox domain	1.9e-30	114.6
1507	Kelch	Kelch motif	1.7e-43	157.9
1508	homeobox	Homeobox domain	1.8e-23	91.4
1512	MIF4G	MIF4G domain	1.7e-37	138.0
1513	zf-AN1	AN1-like Zinc finger	1.5e-18	75.1
1514	SET	SET domain	4.6e-62	219.6
1525	MAGE	MAGE family	0.00054	-70.6
1526	FAD_binding_6	Oxidoreductase FAD-binding domain	3.2e-25	97.2
1527	DENN	DENN (AEX-3) domain	3.5e-29	108.6
1528	DENN	DENN (AEX-3) domain	3.5e-29	108.6

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Table 4A

SEQ ID	Model	Description	E-value	Score
1530	rvt	Reverse transcriptase (RNA-dependent DNA polymerase)	9.7e-08	33.1
1531	myb_DNA-binding	Myb-like DNA-binding domain	4.3e-21	79.1
1532	zf-C2H2	Zinc finger, C2H2 type	5.1e-15	63.3
1534	PH	PH domain	1.5e-50	181.4
1535	PH	PH domain	9.2e-51	182.1
1536	SH3	SH3 domain	0.00014	25.6
1540	Ndr	Ndr family	4.5e-103	355.9
1541	Ribosomal_L35p	Ribosomal protein L35	6e-26	99.6
1546	TPR	TPR Domain	0.0056	23.3
1547	ARID	ARID/BRIGHT DNA binding domain	1.3e-42	154.9
1548	Kelch	Kelch motif	1.2e-31	118.5
1552	GST_N	Glutathione S-transferase, N-terminal domain	2.8e-14	54.5
1554	GTP_EFTU_D2	Elongation factor Tu domain 2	3e-08	34.6
1555	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	0.063	15.2
1556	pkinase	Protein kinase domain	1.9e-35	131.2
1557	pkinase	Protein kinase domain	8.9e-39	142.2
1559	5-FTHF_cyc-lig	5-formyltetrahydrofolate cyclo-ligase family	1.8e-21	84.7
1562	ig	Immunoglobulin domain	9.6e-09	33.2
1563	RasGEF	RasGEF domain	1.7e-88	307.4
1564	RasGEF	RasGEF domain	1.7e-88	307.4
1569	ferritin	Ferritin	2.3e-134	454.1
1570	CUB	CUB domain	3.2e-56	200.2
1571	Kelch	Kelch motif	3.7e-07	37.2
1572	MBD	Methyl-CpG binding domain	0.089	11.8
1573	ubiquitin	Ubiquitin family	5.8e-16	62.5
1576	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.2e-05	20.8
1577	ArfGap	Putative GTP-ase activating protein for Arf	9.7e-47	168.7
1579	filament	Intermediate filament protein	5e-128	438.7
1581	lactamase_B	Metallo-beta-lactamase superfamily	0.014	-6.8
1582	Keratin_B2	Keratin, high sulfur B2 protein	1.3e-06	23.9
1583	ParA	ParA family ATPase	0.0015	5.2
1585	crystall	Beta/Gamma crystallin	3.3e-73	256.6
1587	T-box	T-box	1.4e-89	311.1
1589	LRR	Leucine Rich Repeat	6.7e-11	49.6
1590	60s_ribosomal	60s Acidic ribosomal protein	3.2e-37	121.5
1591	FMO-like	Flavin-binding monooxygenase-like	0	1158.7
1592	FMO-like	Flavin-binding monooxygenase-like	0	1158.7
1594	LIM	LIM domain	6.8e-45	162.6
1597	LRR	Leucine Rich Repeat	0.007	23.0
1600	bromodomain	Bromodomain	4.8e-182	618.2
1601	Armadillo_seg	Armadillo/beta-catenin-like repeat	3.8e-08	40.5
1604	zf-C2H2	Zinc finger, C2H2 type	4e-83	289.6
1609	Gelsolin	Gelsolin repeat.	8.7e-49	175.5
1611	zf-C2H2	Zinc finger, C2H2 type	4.8e-09	43.5
1614	Phytoene_dh	Phytoene dehydrogenase related enzyme	9e-06	-236.5
1615	zf-CCHC	Zinc knuckle	2.4e-18	74.4
1619	zf-AN1	AN1-like Zinc finger	0.00034	26.1

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Table 4A

SEQ ID	Model	Description	E-value	Score
1620	zf-AN1	AN1-like Zinc finger	0.087	6.5
1622	kinesin	Kinesin motor domain	2.3e-112	386.7
1623	WD40	WD domain, G-beta repeat	3.1e-38	140.4
1624	bromodomain	Bromodomain	1.2e-14	55.3
1625	zf-C2H2	Zinc finger, C2H2 type	5.6e-35	129.6
1626	TUDOR	Tudor domain	1.1e-64	228.4
1627	PWI	PWI domain	1.4e-35	131.6
1631	zf-C2H2	Zinc finger, C2H2 type	1.9e-59	210.9
1637	T-box	T-box	6.4e-87	302.2
1640	homeobox	Homeobox domain	6.1e-26	99.6
1645	homeobox	Homeobox domain	1.4e-34	128.3
1646	Keratin_B2	Keratin, high sulfur B2 protein	0.00047	-16.3
1649	HMG_box	HMG (high mobility group) box	4.2e-20	80.2
1651	zf-C2H2	Zinc finger, C2H2 type	1.7e-27	104.8
1652	zf-C2H2	Zinc finger, C2H2 type	3.5e-165	562.1
1656	MAGE	MAGE family	6.7e-22	86.2
1661	zf-C2H2	Zinc finger, C2H2 type	3.8e-89	309.6
1665	homeobox	Homeobox domain	1e-27	105.5
1671	zf-C2H2	Zinc finger, C2H2 type	6.7e-29	109.4
1674	PHD	PHD-finger	1.7e-10	48.3
1678	RNase_PH	3' exoribonuclease family	1.3e-75	264.6
1680	zf-C2H2	Zinc finger, C2H2 type	1.2e-88	307.9
1683	filament	Intermediate filament protein	2.8e-46	167.2
1684	homeobox	Homeobox domain	7.1e-26	99.4
1685	SPRY	SPRY domain	2.2e-22	87.8
1688	HTH_3	Helix-turn-helix	2.9e-09	44.2
1689	SET	SET domain	5.7e-51	182.8
1690	lipocalin	Lipocalin / cytosolic fatty-acid binding protein family	3.2e-16	60.0
1692	zf-C2H2	Zinc finger, C2H2 type	1.3e-74	261.3
1696	Ribosomal_L18e	Eukaryotic ribosomal protein L18	3.3e-08	3.4
1699	kinesin	Kinesin motor domain	1e-30	114.5
1700	zf-C2H2	Zinc finger, C2H2 type	4.3e-16	66.9
1707	DDHD	DDHD domain	4.1e-67	236.4
1709	zf-C2H2	Zinc finger, C2H2 type	7.2e-63	222.3
1710	zf-C2H2	Zinc finger, C2H2 type	1.3e-70	248.0
1711	ERM	Ezrin/radixin/moesin family	8.5e-219	740.3
1712	ERM	Ezrin/radixin/moesin family	8.5e-219	740.3
1713	ERM	Ezrin/radixin/moesin family	8.5e-219	740.3
1714	Ulp1_C	Ulp1 protease family, C-terminal catalytic domain	5.7e-14	59.8
1715	zf-C2H2	Zinc finger, C2H2 type	2.1e-92	320.4
1717	BTB	BTB/POZ domain	6.3e-29	109.5
1718	rvt	Reverse transcriptase (RNA-dependent DNA polymerase)	0.0014	17.6
1723	GCR	Glucocorticoid receptor	5.3e-304	1023.3
1725	AP_endonucleas1	AP endonuclease family 1	2.2e-120	398.9
1728	HLH	Helix-loop-helix DNA-binding domain	0.0055	21.9
1729	SCAN	SCAN domain	5.4e-46	166.2
1731	arginase	Arginase family	9.5e-57	201.9
1732	GLFV_dehydrog_N	Glu/Leu/Phe/Val dehydrogenase, dimerisation domain	2.7e-69	243.6
1734	SH3	SH3 domain	2e-12	54.7
1737	wnt	wnt family	1e-118	327.4

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Table 4A

SEQ ID	Model	Description	E-value	Score
1738	wnt	wnt family	2.4e-124	342.9
1743	G-patch	G-patch domain	1.7e-12	54.9
1744	Kelch	Kelch motif	1.1e-41	151.9
1746	LRR	Leucine Rich Repeat	8.2e-29	109.2
1759	Ski_Sno	SKI/SNO/DAC family	6.7e-56	199.1
1762	ELM2	ELM2 domain	1.6e-09	45.1
1769	WH1	WH1 domain	0.0017	11.6
1770	OLF	Olfactomedin-like domain	8.2e-41	149.0
1772	Kelch	Kelch motif	3.2e-40	147.1
1775	LRR	Leucine Rich Repeat	1e-21	85.6
1776	spectrin	Spectrin repeat	0.037	13.1
1777	dUTPase	dUTPase	2.7e-36	134.0
1778	homeobox	Homeobox domain	1.7e-29	111.4
1790	LRR	Leucine Rich Repeat	1.2e-09	45.5
1792	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	9.7e-102	351.4
1793	FYVE	FYVE zinc finger	1.8e-19	74.1
1801	zf-C2H2	Zinc finger, C2H2 type	4.6e-60	213.0
1807	SH3	SH3 domain	4.6e-15	63.5
1808	pkinase	Protein kinase domain	2.6e-75	263.6
1811	Rhodanese	Rhodanese-like domain	2.4e-65	230.5
1815	zf-C2H2	Zinc finger, C2H2 type	2.5e-16	67.7
1818	zf-C2H2	Zinc finger, C2H2 type	1e-111	384.6
1821	DnaJ	DnaJ domain	5.9e-24	93.0
1823	UQ_con	Ubiquitin-conjugating enzyme	3.8e-49	176.7
1824	zf-C2H2	Zinc finger, C2H2 type	5.5e-112	385.5
1830	zf-C2H2	Zinc finger, C2H2 type	1.2e-59	211.6
1834	SCAN	SCAN domain	5.1e-64	226.1
1838	DM-domain	DM DNA binding domain	3.8e-25	97.0
1846	UBX	UBX domain	7.8e-10	46.1
1849	LIM	LIM domain	9.9e-05	23.0
1852	zf-B_box	B-box zinc finger.	6.6e-08	39.7
1854	mito_carr	Mitochondrial carrier protein	2.9e-64	226.9
1856	zf-C2H2	Zinc finger, C2H2 type	3.4e-50	180.2
1859	TGT	Queuine tRNA-ribosyltransferase	9.7e-19	75.7
1860	Myosin_tail	Myosin tail	4e-99	342.7
1861	LRR	Leucine Rich Repeat	1.2e-09	45.5
1863	trypsin	Trypsin	3.1e-86	274.1
1869	FH2	Formin Homology 2 Domain	1.7e-52	187.8
1873	Josephin	Josephin	3.9e-30	113.0
1874	GTP_EFTU	Elongation factor Tu GTP binding domain	1.5e-19	73.7
1875	GTP_EFTU	Elongation factor Tu GTP binding domain	4.6e-71	249.5
1876	helicase_C	Helicase conserved C-terminal domain	7.6e-19	76.0
1880	KRAB	KRAB box	7.2e-43	155.8
1883	LIM	LIM domain	9.9e-50	178.6
1885	zf-C2H2	Zinc finger, C2H2 type	9.7e-30	112.2
1886	PH	PH domain	7.8e-06	25.8
1888	homeobox	Homeobox domain	1.7e-10	48.3
1890	zf-C2H2	Zinc finger, C2H2 type	1.4e-118	407.3
1891	KRAB	KRAB box	8.5e-05	20.7
1892	MyTH4	MyTH4 domain	7.3e-24	92.7
1895	IF4E	Eukaryotic initiation factor 4E	1.5e-99	344.1

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Table 4A

SEQ ID	Model	Description	E-value	Score
1898	zf-C2H2	Zinc finger, C2H2 type	1.4e-63	224.6
1899	zf-C4	Zinc finger, C4 type (two domains)	2.1e-16	58.9
1903	HEAT	HEAT repeat	5.6e-13	56.6
1913	homeobox	Homeobox domain	0.0037	19.9
1917	kinesin	Kinesin motor domain	2.1e-64	227.4
1918	zf-C4	Zinc finger, C4 type (two domains)	3.6e-16	58.2
1921	rnaseH	RNase H	2.4e-20	77.7
1924	Ribosomal_S8	Ribosomal protein S8	3.1e-37	124.7
1926	zf-C2H2	Zinc finger, C2H2 type	1.2e-69	244.8
1927	filament	Intermediate filament protein	1.7e-119	410.4
1928	zf-C2H2	Zinc finger, C2H2 type	2.1e-67	237.3
1929	zf-C2H2	Zinc finger, C2H2 type	6e-155	528.2
1930	zf-C2H2	Zinc finger, C2H2 type	1.3e-95	331.0
1932	zf-C2H2	Zinc finger, C2H2 type	2.2e-36	134.3
1933	zf-C2H2	Zinc finger, C2H2 type	3.3e-117	402.8
1936	HLH	Helix-loop-helix DNA-binding domain	2e-21	84.6
1937	zf-C2H2	Zinc finger, C2H2 type	9.4e-160	544.1
1938	CUB	CUB domain	1.4e-37	138.2
1939	sushi	Sushi domain (SCR repeat)	1.3e-09	45.4
1941	IBR	IBR domain	0.0027	14.2
1942	Ribosomal_S4	Ribosomal protein S4/S9 N-terminal domain	1.2e-26	101.9

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Table 4B

SEQ ID	Model	Description	E-value	Score	Repeats	Position
972	globin	Globin	1.6e-41	151.4	1	2-122
973	arginase	Arginase family	1.1e-159	543.9	1	4-290
974	arginase	Arginase family	1.1e-156	533.9	1	4-290
975	arginase	Arginase family	2.5e-167	569.3	1	4-289
979	PID	Phosphotyrosine interaction domain (PTB/PID)	3.3e-105	362.9	2	420-558:593-715
979	WW	WW domain	2.3e-09	44.5	1	293-321
980	PID	Phosphotyrosine interaction domain (PTB/PID)	3.3e-105	362.9	2	399-537:572-694
980	WW	WW domain	2.3e-09	44.5	1	293-321
981	zf-C4	Zinc finger, C4 type (two domains)	6.3e-39	142.8	1	9-84
983	Exonuclease	Exonuclease	2.2e-21	84.5	1	7-149
986	ank	Ankyrin repeat	2.5e-39	144.1	7	17-51:52-84:85-117:118-150:151-183:184-216:217-252
987	zf-C2H2	Zinc finger, C2H2 type	3.2e-119	409.5	14	215-237:243-265:271-293:299-321:327-349:355-377:383-405:411-433:439-461:467-489:495-517:523-545:551-573:579-601
987	KRAB	KRAB box	5.8e-27	103.0	1	8-48
987	zf-BED	BED zinc finger	2.3	-1.6	1	284-322
987	TFIIS	Transcription factor S-II (TFIIS)	2.7	-2.4	1	467-505
987	LIM	LIM domain	4.2	-17.0	1	553-602
987	PHD	PHD-finger	6	-17.1	1	412-475
987	zf-TRAF	TRAF-type zinc finger	6.4	-7.8	1	261-315
989	CUB	CUB domain	4.4e-20	80.1	1	7-113
989	LCCL	LCCL domain	2.4e-06	31.8	1	116-207
989	F5_F8_type_C	F5/8 type C domain	3.4e-06	18.2	1	278-398
990	FKBP	FKBP-type peptidyl-prolyl cis-trans isomeras	2.9e-28	107.3	1	175-263
992	cpn60_TCP1	TCP-1/cpn60 chaperonin family	1e-138	474.2	1	30-481
992	Methylase_M	Type I restriction modification system, M	8.5	-137.7	1	176-358
994	WD40	WD domain, G-beta repeat	3.7e-31	116.9	10	8-44:51-87:93-129:137-172:187-222:228-264:279-

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Table 4B

						313:429- 465:476- 512:518-554
995	LIM_bind	LIM-domain binding protein	7e-298	1003.0	1	37-411
997	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	9.3e-26	99.0	1	1194-1254
997	UCH-1	Ubiquitin carboxyl-terminal hydrolases famil	7.4e-13	56.2	1	422-453
998	Transposase_22	L1 transposable element	3e-06	-69.2	1	1-228
998	Herpes_UL14	Herpesvirus UL14-like protein	9.7	-92.7	1	26-151
999	FAD-oxidase_C	FAD linked oxidases, C-terminal domain	1.7e-91	317.4	1	335-576
999	FAD_binding_4	FAD binding domain	2.2e-61	217.4	1	136-321
1007	myb_DNA-binding	Myb-like DNA-binding domain	9.3e-09	42.5	1	67-114
1007	ZZ	Zinc finger, ZZ type	0.021	17.8	1	4-47
1008	proteasome	Proteasome A-type and B-type	2.2e-38	140.9	1	74-269
1009	myb_DNA-binding	Myb-like DNA-binding domain	1.3	10.9	1	149-199
1011	DnaJ	DnaJ domain	1e-15	65.6	1	14-109
1012	Fe_hyd_lg_C	Iron only hydrogenase large subunit, C-te	6e-156	531.5	1	36-337
1012	Fe_hyd_SS_U	Iron hydrogenase small subunit	0.46	-2.3	1	343-398
1014	rrm	RNA recognition motif.	1.5e-20	81.7	1	36-106
1015	TPR	TPR Domain	1.9e-18	74.7	7	326-359:399- 443:478- 511:623- 656:657- 690:691- 724:725-758
1015	sodfe	Iron/manganese superoxide dismutases, alpha-	5.1	-36.4	1	143-217
1018	tubulin	Tubulin/FtsZ family	7.3e-281	946.5	1	2-449
1019	tRNA-synt_2	tRNA synthetases class II (D, K and N)	3.2e-170	578.9	1	315-637
1019	tRNA_anti	OB-fold nucleic acid binding domain	4.1e-12	53.7	1	200-285
1019	tRNA-synt_2d	tRNA synthetases class II core domain	0.75	-141.6	1	338-627
1019	tRNA-synt_2b	tRNA synthetase class II core domain	3.1	-50.5	1	323-461
1020	Armadillo_seg	Armadillo/beta-catenin-like repeat	0.55	16.7	2	130-170:181-220
1020	DUF71	Domain of unknown function DUF71	5.4	-130.7	1	124-295
1022	abhydrolase	alpha/beta hydrolase fold	4.5e-20	80.1	1	95-338
1022	Thioesterase	Thioesterase domain	2.5	-46.0	1	69-341
1025	zf-C2H2	Zinc finger, C2H2 type	4.2e-73	256.3	9	230-252:258- 280:286- 308:314- 336:342- 364:370- 392:398-

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Table 4B

						420:426- 448:454-476
1025	KRAB	KRAB box	2e-23	91.2	1	39-77
1025	zf-BED	BED zinc finger	1.6	-0.4	1	355-393
1025	E6	Early Protein (E6)	9.8	-69.5	1	316-403
1026	efhand	EF hand	0.56	16.7	1	483-511
1027	PCI	PCI domain	1.1e-13	58.9	1	88-168
1028	PCI	PCI domain	0.0097	20.6	1	88-150
1028	DUF66	Protein of unknown function DUF66	8.8	-201.6	1	1-220
1029	ParBc	ParB-like nuclease domain	0.033	7.3	1	42-135
1030	Pribosyltran	Phosphoribosyl transferase domain	5.1e-17	70.0	1	170-338
1032	ig	Immunoglobulin domain	7.7e-06	32.8	2	269-350:505- 570
1032	KRAB	KRAB box	7	-4.0	1	82-127
1033	rrm	RNA recognition motif.	3.2e-41	150.4	3	164-236:245- 304:305-368
1033	Collagen	Collagen triple helix repeat (20 copies)	6.8	-65.1	1	467-525
1034	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.7e-13	56.8	1	18-56
1034	PHD	PHD-finger	8	-18.2	1	17-59
1035	DUF289	Putative membrane protein	1.7e-57	204.5	1	113-372
1037	HSP20	Hsp20/alpha crystallin family	8.2e-10	46.0	1	155-251
1039	LRR	Leucine Rich Repeat	1.7e-09	45.0	3	54-75:76- 97:98-122
1040	LRR	Leucine Rich Repeat	1.7e-09	45.0	3	54-75:76- 97:98-122
1041	Ribosomal_ L28e	Ribosomal L28e protein family	1.4e-65	231.3	1	2-171
1042	FKBP	FKBP-type peptidyl-prolyl cis-trans iso	8.3e-21	82.6	1	189-287
1042	Lipoprotein 7	Adhesin lipoprotein	0.16	-96.7	1	359-830
1042	WH1	WH1 domain	0.36	-13.3	1	69-171
1042	filament	Intermediate filament protein	7.3	-207.1	1	572-783
1042	Peptidase_S 21	Assemblin (Peptidase family S21)	10	-174.4	1	229-472
1043	GST_C	Glutathione S-transferase, C- terminal domain	1.5e-31	118.2	1	65-174
1043	GST_N	Glutathione S-transferase, N- terminal domain	1.4e-15	65.2	1	4-59
1043	TUDOR	Tudor domain	8	-19.2	1	72-183
1044	GST_N	Glutathione S-transferase, N- terminal domain	8.3e-26	99.2	1	4-77
1044	GST_C	Glutathione S-transferase, C- terminal domain	2.5e-22	87.6	1	62-171
1045	GST_N	Glutathione S-transferase, N- terminal domain	8.3e-26	99.2	1	4-77
1045	GST_C	Glutathione S-transferase, C- terminal domain	9.8e-12	52.4	1	83-174
1047	adh_zinc	Zinc-binding dehydrogenase	1.1e-91	318.0	1	14-332
1047	GFO_IDH_ MocA	Oxidoreductase family, NAD- binding Rossm	9	-40.2	1	156-257
1054	SAICAR_sy nt	SAICAR synthetase	7.3e-111	381.7	1	9-235

Table 4B

1054	AIRC	AIR carboxylase	2.1e-71	250.7	1	248-402
1056	HupF_HypC	HupF/HypC family	4	-30.6	1	79-145
1058	KE2	KE2 family protein	3.6	-43.3	1	89-186
1059	P35	Apoptosis preventing protein	5.8	-105.3	1	67-376
1059	Tropomyosin	Tropomyosin	8.7	-119.9	1	319-504
1059	Lipase_chap	Proteobacterial lipase chaperone protein	9.2	-132.4	1	208-490
1061	zf-C2H2	Zinc finger, C2H2 type	5.5e-159	541.6	22	105-127:133-155:161-183:189-211:217-239:245-267:273-295:301-323:329-351:357-379:385-407:413-435:441-463:469-491:497-519:553-575:581-603:609-631:637-659:665-687:693-715:721-743
1061	HNH	HNH endonuclease	0.39	11.9	1	245-298
1061	TFIIS	Transcription factor S-II (TFIIS)	0.64	3.0	1	220-255
1061	zf-BED	BED zinc finger	0.99	1.6	1	453-492
1061	FYVE	FYVE zinc finger	7.9	-25.2	1	545-623
1061	DC1	DC1 domain	8.8	1.6	1	385-428
1061	LIM	LIM domain	9.7	-20.0	1	219-287
1064	zf-C2H2	Zinc finger, C2H2 type	1.1e-159	543.8	21	190-212:218-240:246-268:274-296:302-324:330-352:358-380:386-408:414-436:442-464:470-492:498-520:526-548:554-576:582-604:610-632:638-660:666-688:694-716:722-744:750-772

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Table 4B

1064	FYVE	FYVE zinc finger	2.5	-20.3	1	377-453
1064	HNH	HNH endonuclease	3.5	3.7	1	330-383
1064	TFIIS	Transcription factor S-II (TFIIS)	4	-3.8	1	638-676
1064	zf-BED	BED zinc finger	6.7	-5.8	1	371-409
1064	LIM	LIM domain	8.5	-19.5	1	332-384
1065	HTH_7	Helix-turn-helix domain of resolvase	7.1	2.4	1	18-60
1069	Myosin tail	Myosin tail	2.2	-491.1	1	5-474
1069	ERM	Ezrin/radixin/moesin family	3.5	-212.6	1	150-461
1069	filament	Intermediate filament protein	4	-200.5	1	29-305
1069	Lipoprotein 7	Adhesin lipoprotein	7.2	-127.3	1	11-454
1074	pkinase	Protein kinase domain	2e-12	44.2	1	1-182
1076	zf-C2H2	Zinc finger, C2H2 type	3.4e-13	57.2	4	215-239:275-299:380-404:926-948
1076	homeobox	Homeobox domain	0.82	-12.8	1	841-909
1077	zf-C2H2	Zinc finger, C2H2 type	8.8e-11	49.2	4	81-103:108-130:136-159:982-1004
1077	PHD	PHD-finger	3.7	-15.1	1	5-89
1077	Rad10	DNA repair protein rad10	8	-28.5	1	360-415
1084	NUDIX	NUDIX domain	0.0011	21.7	1	19-161
1087	UPF0079	Uncharacterised P-loop hydrolase UPF0079	6.7	-61.4	1	54-150
1089	zf-C2H2	Zinc finger, C2H2 type	4.1e-189	641.7	26	108-130:136-158:164-186:192-214:220-242:248-270:276-298:304-326:332-354:360-382:388-410:416-438:444-466:472-494:500-522:528-550:556-578:584-606:612-634:640-662:668-690:696-718:724-746:752-774:780-801:807-829
1089	zf-TRAF	TRAF-type zinc finger	1.1	0.7	1	438-488
1089	PHD	PHD-finger	3.3	-14.6	1	249-312
1089	zf-BED	BED zinc finger	3.9	-3.8	1	792-830
1089	zf-MIZ	MIZ zinc finger	6	-19.7	1	678-735
1089	DM-domain	DM DNA binding domain	7.1	-11.9	1	526-576

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Table 4B

1089	TFIIS	Transcription factor S-II (TFIIS)	7.5	-6.1	1	640-678
1089	Metallothio PEC	Plant PEC family metallothionein	7.9	-40.4	1	137-199
1089	DC1	DC1 domain	9	1.5	1	248-289
1090	PX	PX domain	3.1e-17	70.7	1	78-187
1093	cyclin	Cyclin, N-terminal domain	1.2e-45	165.1	1	148-275
1093	cyclin_C	Cyclin, C-terminal domain	1.7e-18	74.9	1	277-406
1095	A1pp	Appr-1"-p processing enzyme family	1.6e-38	141.4	2	229-347:441- 558
1095	WWE	WWE domain	3.3e-23	90.5	1	932-1010
1096	60s_riboso mal	60s Acidic ribosomal protein	1.6e-27	104.9	1	20-131
1103	C2	C2 domain	3.6e-21	83.8	2	42-126:173- 258
1105	CAP_GLY	CAP-Gly domain	8e-26	99.2	1	148-190
1106	Band_41	FERM domain (Band 4.1 family)	2.1e-104	360.2	1	99-288
1107	Band_41	FERM domain (Band 4.1 family)	2.1e-104	360.2	1	99-288
1108	PHD	PHD-finger	2.7	-13.8	1	798-833
1110	WD40	WD domain, G-beta repeat	1.8e-10	48.2	4	93-129:266- 308:313- 352:413-449
1114	IQ	IQ calmodulin-binding motif	0.013	22.1	1	118-138
1115	zf-C2H2	Zinc finger, C2H2 type	1.5e-76	267.7	11	195-217:223- 245:251- 273:279- 301:307- 329:335- 357:363- 385:391- 413:419- 441:447- 469:475-497
1115	KRAB	KRAB box	5.2e-23	89.9	1	7-47
1115	zf-BED	BED zinc finger	1.4	0.3	1	236-274
1115	PHD	PHD-finger	3.2	-14.6	1	196-259
1115	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.5	-6.1	1	365-396
1115	ThiC	ThiC family	6.4	-344.2	1	12-295
1115	LIM	LIM domain	8.5	-19.6	1	365-424
1115	rubredoxin	Rubredoxin	9.6	-11.9	1	444-487
1116	Kelch	Kelch motif	1.5e-45	164.8	6	262-313:315- 361:363- 408:410- 455:457- 509:516-561
1116	BTB	BTB/POZ domain	3.7e-23	90.4	1	20-129
1117	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0022	23.3	1	277-315
1118	zf-C2H2	Zinc finger, C2H2 type	2.4e-29	110.9	5	368-390:396- 418:424- 446:476- 498:504-526
1118	KRAB	KRAB box	4.1e-13	57.0	1	213-254
1118	PHD	PHD-finger	5.2	-16.5	1	477-512

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1118	LIM	LIM domain	5.3	-17.8	1	370-424
1119	Band_7	SPFH domain / Band 7 family	3.2e-38	140.4	1	39-243
1122	zf-C2H2	Zinc finger, C2H2 type	4.4e-107	369.2	13	141-163:169-191:197-219:225-247:253-275:281-303:309-331:337-359:365-387:393-415:421-443:449-471:477-499
1122	zf-BED	BED zinc finger	0.6	3.5	2	154-192:266-304
1122	PHD	PHD-finger	5.2	-16.5	1	170-233
1122	LIM	LIM domain	7.5	-19.1	1	171-235
1122	TFIIS	Transcription factor S-II (TFIIS)	7.6	-6.1	1	253-291
1124	tRNA-synt_1c	tRNA synthetases class I (E and Q)	7.4e-114	391.7	1	36-521
1124	tRNA-synt_1d	tRNA synthetases class I (R)	4.2	-152.6	1	6-336
1124	tRNA-synt_1f	tRNA synthetases class I (K)	4.7	-369.7	1	37-517
1126	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	4.8e-21	83.3	1	86-180
1126	W2	eIF4-gamma/eIF5/eIF2-epsilon	6.7	-26.5	1	360-440
1128	PAX	'Paired box' domain	4.4e-89	309.4	1	74-198
1129	ENT	ENT domain	9.7e-17	69.0	1	16-88
1132	SH3	SH3 domain	0.0021	16.2	1	11-67
1132	ArsA_ATPase	Anion-transporting ATPase	3.7	-189.9	1	585-821
1132	Cdc37	Cdc37 family	6.2	-123.5	1	1558-1774
1132	DUF262	Protein of unknown function DUF262	6.9	-64.7	1	625-871
1135	PHD	PHD-finger	0.7	-8.4	2	81-131:279-329
1136	DUF71	Domain of unknown function DUF71	6.8e-83	288.8	1	1-242
1137	SCP	SCP-like extracellular protein	4e-08	-6.3	1	1-115
1138	Tropomodulin	Tropomodulin	3.7e-179	608.6	1	30-308
1139	Ribosomal_L44	Ribosomal protein L44	7.5e-41	149.1	1	17-95
1141	RCC1	Regulator of chromosome condensation (RCC1)	0.00096	25.9	2	176-225:318-371
1144	RUN	RUN domain	0.00018	24.8	1	191-372
1148	ank	Ankyrin repeat	1.4e-29	111.7	5	503-536:537-574:576-608:609-642:643-677
1148	Remorin_C	Remorin, C-terminal region	4.4	-40.9	1	214-311
1149	chromo	'chromo'	4e-23	90.2	1	9-49
1149	AT_hook	AT hook motif	0.9	13.9	1	74-86

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1149	Arte_nucleo cap	Arterivirus nucleocapsid protein	6.4	-31.5	1	162-270
1152	DEAD	DEAD/DEAH box helicase	5	-75.3	1	218-391
1153	CH	Calponin homology (CH) domain	2.4e-29	110.9	1	2-108
1153	LIM	LIM domain	8.5e-05	22.7	1	164-222
1153	Stathmin	Stathmin family	6.6	-18.2	1	650-788
1156	efhand	EF hand	7e-20	79.5	5	119-147:155- 183:244- 272:285- 313:321-349
1157	DUF232	Putative transcriptional regulator	0.9	-17.6	1	92-211
1157	K-box	K-box region	3.2	-37.0	1	133-206
1159	DSPc	Dual specificity phosphatase, catalytic	0.00019	0.9	1	66-205
1159	Y_phosphat ase	Protein-tyrosine phosphatase	6.7	-88.7	1	29-192
1160	Keratin_B2	Keratin, high sulfur B2 protein	3.9	-77.5	1	160-275
1161	zf-C2H2	Zinc finger, C2H2 type	1.6e-30	114.8	5	356-378:384- 406:412- 434:440- 462:468-490
1161	SCAN	SCAN domain	3e-23	90.7	1	38-129
1161	PHD	PHD-finger	2.4	-13.3	1	357-420
1161	zf-BED	BED zinc finger	7.3	-6.1	1	425-463
1162	C1q	C1q domain	0.0001	2.0	1	367-506
1162	Collagen	Collagen triple helix repeat (20 copies)	0.048	-23.2	1	298-356
1164	kinesin	Kinesin motor domain	2e-156	533.1	1	72-356
1164	Ribosomal_ L35p	Ribosomal protein L35	6	-22.0	1	847-892
1165	C2	C2 domain	0.087	5.3	1	368-456
1166	spectrin	Spectrin repeat	2.2	-13.2	1	144-246
1166	Bac_globin	Protozoan/cyanobacterial globin	7.1	-58.3	1	63-163
1168	UBX	UBX domain	0.013	15.3	1	390-470
1169	KRAB	KRAB box	3.3e-25	97.2	1	14-54
1172	zf-C2H2	Zinc finger, C2H2 type	9.1e-59	208.7	8	158-180:186- 208:214- 236:242- 264:270- 292:298- 320:326- 348:354-376
1172	KRAB	KRAB box	4e-22	86.9	1	23-63
1172	E6	Early Protein (E6)	3.3	-63.9	1	216-303
1173	NUDIX	NUDIX domain	0.0038	16.4	1	19-157
1174	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5	2	18-40:46-68
1176	zf-C2H2	Zinc finger, C2H2 type	6.6e-07	36.4	3	109-133:140- 162:289-311
1178	Guanylate_k in	Guanylate kinase	0.58	-34.1	1	246-334
1179	EMP24_GP 25L	emp24/gp25L/p24 family	0.06	-40.8	1	1-129
1180	RhoGEF	RhoGEF domain	6.5e-15	63.0	1	179-358
1180	PH	PH domain	1.6e-06	35.1	1	392-503

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1180	SH3	SH3 domain	2.6e-05	31.1	1	523-573
1181	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.018	15.4	1	715-764
1184	actin	Actin	0.59	-64.0	1	112-500
1185	ig	Immunoglobulin domain	4.2e-47	169.9	5	306-366:521-581:1545-1605:1742-1803:1876-1936
1185	PX	PX domain	2.8	-14.9	1	768-883
1186	FYVE	FYVE zinc finger	8.2e-19	75.9	1	1168-1232
1186	RUN	RUN domain	0.067	-8.4	1	36-166
1186	Tropomyosin	Tropomyosin	0.098	-85.8	1	868-1098
1186	STAT	STAT protein, all-alpha domain	1.5	-59.4	1	978-1154
1186	filament	Intermediate filament protein	2.4	-194.4	1	398-711
1186	K-box	K-box region	3.3	-37.2	1	623-718
1186	ERM	Ezrin/radixin/moesin family	3.6	-212.7	1	377-680
1186	Myosin_tail	Myosin tail	3.9	-515.5	1	219-1083
1186	Remorin_C	Remorin, C-terminal region	5.8	-42.3	1	650-763
1186	Apolipoprotein	Apolipoprotein A1/A4/E family	5.9	-113.6	1	841-1076
1186	bZIP	bZIP transcription factor	9.4	-7.0	1	980-1034
1186	Peptidase_M41	Peptidase family M41	9.6	-175.7	1	746-845
1187	Apolipoprotein	Apolipoprotein A1/A4/E family	9	-117.8	1	47-248
1188	globin	Globin	4e-38	140.1	1	14-160
1190	Adenylosucc synt	Adenylosuccinate synthetase	0	1075.1	1	32-455
1191	Rhodanese	Rhodanese-like domain	3.9e-07	37.1	1	290-390
1191	DnaJ_CXX CXGXXG	DnaJ central domain (4 repeats)	3.4	-46.0	1	409-467
1193	adh_zinc	Zinc-binding dehydrogenase	2.3e-80	280.4	1	56-387
1193	Semialdehyde dh	Semialdehyde dehydrogenase, NAD bindin	3.8	-50.3	1	196-312
1194	MMPL	MMPL family	7	-38.9	1	304-397
1196	DUF279	Eukaryotic protein of unknown function, DUF2	2e-46	167.7	1	68-196
1202	F-box	F-box domain	1.1e-05	32.3	1	671-718
1202	zf-TRAF	TRAF-type zinc finger	2.6	-3.4	1	67-137
1203	spectrin	Spectrin repeat	2.9	-14.6	1	22-135
1204	zf-C2H2	Zinc finger, C2H2 type	6.3e-34	126.1	5	14-36:42-64:70-94:100-122:130-152
1204	zf-TRAF	TRAF-type zinc finger	5.8	-7.3	1	36-88
1205	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	2.3e-12	54.5	1	34-72
1206	MARCKS	MARCKS family	3.4	-88.2	1	185-442
1212	zf-C2H2	Zinc finger, C2H2 type	2.2e-24	94.5	7	69-92:230-253:287-310:359-382:486-508:519-542:618-640

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1212	zf-BED	BED zinc finger	3.9	-3.8	1	336-383
1213	COX6B	Cytochrome oxidase c subunit VIb	4.9e-59	209.5	1	8-85
1214	Sec7	Sec7 domain	8.7e-105	361.5	1	58-243
1214	PH	PH domain	9.7e-24	92.3	1	260-348
1218	PyrI_C	Aspartate carbamoyltransferase regulatory ch	6.5	-14.3	1	65-95
1219	ZZ	Zinc finger, ZZ type	6.7e-10	46.3	1	38-82
1219	zf-B_box	B-box zinc finger	2.3	-3.6	1	39-84
1219	DC1	DC1 domain	6.7	2.6	1	42-68
1219	UBA	UBA/TS-N domain	6.9	12.7	1	291-332
1220	zf-CXXC	CXXC zinc finger	1.2e-15	65.4	1	257-303
1220	F-box	F-box domain	2.2e-08	41.3	2	581-629:738-786
1220	PHD	PHD-finger	0.01	8.6	1	313-372
1223	filament	Intermediate filament protein	3.8	-199.7	1	45-272
1224	HMG_box	HMG (high mobility group) box	6e-18	73.1	1	81-149
1225	zf-C2H2	Zinc finger, C2H2 type	1.5e-75	264.4	9	267-289:295-317:323-345:351-373:379-401:407-429:435-457:463-485:491-513
1225	SCAN	SCAN domain	3.5e-41	150.2	1	44-121
1225	zf-BED	BED zinc finger	0.51	4.2	1	448-486
1225	GATA	GATA zinc finger	1.1	-4.8	1	461-507
1226	Kelch	Kelch motif	8.1e-19	75.9	3	30-82:87-132:137-182
1227	Kelch	Kelch motif	7e-21	82.8	4	30-82:88-133:138-183:188-233
1228	DENN	DENN (AEX-3) domain	6.7e-82	285.5	1	116-298
1228	dDENN	dDENN domain	4e-25	96.9	1	351-420
1228	uDENN	uDENN domain	8.9e-22	85.8	1	1-86
1228	GRAM	GRAM domain	1.5e-10	48.5	1	871-957
1229	zf-C2H2	Zinc finger, C2H2 type	2.2e-59	210.7	8	159-181:187-209:215-237:243-265:271-293:299-321:327-349:355-377
1229	KRAB	KRAB box	1.1e-24	95.5	1	8-48
1229	GATA	GATA zinc finger	2.3	-7.4	1	157-203
1229	zf-BED	BED zinc finger	6.5	-5.7	2	284-322:340-378
1230	Nebulin	Nebulin repeat	1.7e-62	221.0	9	174-202:209-237:245-273:315-343:354-382:389-417:425-453:493-

Table 4B

						521:528-555
1230	LIM	LIM domain	5.9e-05	24.0	1	6-62
1231	TPR	TPR Domain	1.3e-05	32.0	2	103-136:224-257
1235	BRCT	BRCA1 C Terminus (BRCT) domain	5e-07	36.8	2	2-90:121-209
1236	zf-B_box	B-box zinc finger	1.4e-07	38.6	1	121-163
1236	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0022	23.2	1	26-81
1236	PHD	PHD-finger	0.28	-4.8	1	25-84
1236	zf-MIZ	MIZ zinc finger	8.7	-20.9	1	24-87
1238	mito_carr	Mitochondrial carrier protein	3.7e-74	259.8	3	12-107:108-203:206-299
1239	Armadillo_seg	Armadillo/beta-catenin-like repeat	3.2e-07	37.4	5	461-503:617-662:670-705:706-746:747-790
1239	VPS9	Vacuolar sorting protein 9 (VPS9) domain	7.6	-37.0	1	334-428
1240	mbt	mbt repeat	1.5e-123	423.9	3	88-161:196-269:300-369
1240	SAM	SAM domain (Sterile alpha motif)	8.9e-11	49.2	1	532-596
1240	zf-C2HC	Zinc finger, C2HC type	2.3e-05	31.3	1	375-407
1240	SAM_PNT	Sterile alpha motif (SAM)/Pointed domain	0.43	-14.4	1	510-599
1241	TT_ORF2	TT viral ORF2	1.6	-88.5	1	147-266
1243	BTB	BTB/POZ domain	5.7e-24	93.1	1	351-460
1243	zf-C2H2	Zinc finger, C2H2 type	1.6e-08	41.8	2	695-717:723-745
1243	K_tetra	K ⁺ channel tetramerisation domain	0.75	-32.6	1	363-457
1243	FYVE	FYVE zinc finger	7.2	-24.8	1	717-787
1243	ZZ	Zinc finger, ZZ type	7.6	-3.9	1	747-792
1245	TruB_N	TruB family pseudouridylate synthase	5.8e-45	162.8	1	103-255
1247	zf-C2H2	Zinc finger, C2H2 type	3e-98	339.8	12	151-173:179-201:207-229:235-257:263-285:291-313:319-341:347-369:375-397:403-425:431-453:459-481
1247	zf-BED	BED zinc finger	0.71	2.9	1	192-230
1247	zf-TRAF	TRAF-type zinc finger	7.5	-8.6	1	309-362
1247	LIM	LIM domain	8.9	-19.7	1	153-217
1248	helicase_C	Helicase conserved C-terminal domain	2.7e-23	90.8	1	154-225
1249	MAGE	MAGE family	1.4e-15	65.2	1	1-200
1250	Collagen	Collagen triple helix repeat (20 copies)	6.1	-64.2	1	40-99
1253	C2	C2 domain	1.9e-27	104.6	1	999-1097
1253	PDZ	PDZ domain (Also known as	9.7e-09	42.5	1	792-879

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Table 4B

		DHR or GLGF)				
1253	OAR	OAR domain	7.8	2.7	1	594-613
1253	Tymo_45kd 70kd	Tymovirus 45/70Kd protein	7.9	-301.5	1	590-974
1254	C2	C2 domain	1.4e-32	121.7	1	999-1088
1254	PDZ	PDZ domain (Also known as DHR or GLGF)	9.7e-09	42.5	1	792-879
1254	OAR	OAR domain	7.8	2.7	1	594-613
1254	Tymo_45kd 70kd	Tymovirus 45/70Kd protein	7.9	-301.5	1	590-974
1255	KH-domain	KH domain	5.1e-42	153.0	3	46-92:124- 173:367-415
1256	ig	Immunoglobulin domain	6.5e-06	33.1	2	8-93:203-281
1259	DUF305	Domain of unknown function	6	-14.5	1	1001-1047
1259	Myosin_tail	Myosin tail	7.2	-542.1	1	878-1729
1259	filament	Intermediate filament protein	9	-209.5	1	1262-1547
1259	HR1	Hr1 repeat	9.9	-4.9	1	183-256
1261	SH2	SH2 domain	4.7e-20	80.1	1	341-417
1263	TPR	TPR Domain	4.3e-05	30.4	2	290-323:324- 357
1267	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.2e-08	42.1	1	164-202
1268	UCR_14kD	Ubiquinol-cytochrome C reductase complex 14k	2.5	-39.3	1	284-382
1268	filament	Intermediate filament protein	4.7	-202.2	1	378-635
1268	Tektin	Tektin family	9.6	-244.7	1	412-738
1272	UBX	UBX domain	3.2e-29	110.5	1	454-534
1272	UIM	Ubiquitin interaction motif	2.3	14.3	1	331-348
1273	GTF2I	GTF2I-like repeat	6.3e-40	146.1	1	107-181
1275	WD40	WD domain, G-beta repeat	0.0042	23.8	1	219-255
1277	BTB	BTB/POZ domain	9.1e-26	99.0	1	38-142
1277	zf-C2H2	Zinc finger, C2H2 type	2e-06	34.8	2	411-433:438- 460
1278	zf-C2H2	Zinc finger, C2H2 type	4.1e-59	209.8	11	23-45:51- 73:79- 101:107- 130:200- 222:228- 250:331- 352:358- 381:414- 436:442- 464:470-492
1278	LIM	LIM domain	3.2	-16.0	1	416-470
1278	Ribosomal_ L34e	Ribosomal protein L34e	5.8	-36.3	1	21-94
1279	fn3	Fibronectin type III domain	5.9	-4.5	1	231-312
1282	PHD	PHD-finger	7.3e-14	59.5	2	205-253:314- 371
1282	DC1	DC1 domain	0.45	12.6	1	313-342
1285	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	2e-18	74.6	1	280-341
1285	UCH-1	Ubiquitin carboxyl-terminal hydrolases famil	5.5e-10	46.6	1	80-111
1287	PP2C	Protein phosphatase 2C	1.6e-16	68.3	1	97-431
1288	PP2C	Protein phosphatase 2C	1.4e-08	35.7	1	26-346
1292	Tymo_45kd	Tymovirus 45/70Kd protein	7.5	-301.0	1	92-465

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Table 4B

	70kd					
1294	BPL_LipA_LipB	Biotin/lipoate A/B protein ligase famil	2e-21	84.6	1	55-178
1295	crystall	Beta/Gamma crystallin	8.4e-95	328.4	2	191-270:277-358
1297	DUF257	Pyrococcus protein of unknown function, DUF2	7.7	-106.7	1	280-457
1298	PNPase	Polyribonucleotide nucleotidyltransferase, R	1.6	-18.1	1	529-596
1298	spectrin	Spectrin repeat	6.2	-18.5	1	464-554
1298	Tektin	Tektin family	7	-241.7	1	414-756
1298	K-box	K-box region	7.5	-41.5	1	512-589
1299	ank	Ankyrin repeat	2.9e-42	153.8	5	67-99:100-132:133-165:166-198:199-231
1301	fn3	Fibronectin type III domain	3.7e-07	37.2	1	359-445
1301	TDH	Vibrio thermostable direct hemolysin	3.5	-33.5	1	431-593
1302	K_tetra	K ⁺ channel tetramerisation domain	6.2e-09	43.1	1	12-111
1307	zf-MYND	MYND finger	3e-09	44.1	1	183-226
1309	Syntaxin	Syntaxin	4.1	-15.3	1	31-213
1311	Ribosomal_L24e	Ribosomal protein L24e	5.4e-50	179.5	1	24-94
1312	Somatomedin_B	Somatomedin B domain	6.4	-7.8	1	430-474
1314	WD40	WD domain, G-beta repeat	4.5e-21	83.4	5	488-524:536-581:655-692:698-734:743-779
1315	Aldose_epim	Aldose 1-epimerase	1.3e-140	480.5	1	20-338
1318	Collagen	Collagen triple helix repeat (20 copies)	7.3	-65.8	1	303-361
1319	zf-C2H2	Zinc finger, C2H2 type	4.8e-92	319.2	12	203-225:231-253:259-281:287-309:315-337:343-365:371-393:399-421:427-449:455-477:483-505:511-533
1319	KRAB	KRAB box	1.3e-26	101.9	1	27-67
1319	zf-BED	BED zinc finger	0.43	4.8	1	244-282
1319	LIM	LIM domain	1.5	-13.1	1	429-488
1319	TFIIS	Transcription factor S-II (TFIIS)	6.2	-5.3	1	290-325
1322	zf-C2H2	Zinc finger, C2H2 type	2	14.8	1	25-49
1324	Ribosomal_S10	Ribosomal protein S10p/S20e	5e-29	109.9	1	19-96
1325	homeobox	Homeobox domain	6.4e-60	212.5	3	546-602:808-864:1016-1072

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Table 4B

1325	zf-C2H2	Zinc finger, C2H2 type	4.3e-15	63.6	7	141-165:198-222:430-453:620-642:719-741:1401-1424:1445-1469
1327	ank	Ankyrin repeat	1.2e-21	85.4	3	31-63:64-96:97-129
1327	SAM	SAM domain (Sterile alpha motif)	0.002	24.8	1	341-403
1329	bZIP	bZIP transcription factor	1.2	2.1	1	82-144
1329	Tropomyosin	Tropomyosin	3.1	-112.0	1	72-316
1329	Transposase 8	Transposase	5.5	-15.9	1	181-259
1329	filament	Intermediate filament protein	8.6	-209.0	1	53-301
1330	zf-C2H2	Zinc finger, C2H2 type	7.1e-91	315.3	13	263-285:291-313:319-341:347-369:375-397:403-425:431-453:459-481:487-509:515-537:543-565:571-593:627-647
1330	KRAB	KRAB box	2.1e-27	104.5	1	8-48
1330	TFIIS	Transcription factor S-II (TFIIS)	4.2	-4.0	1	431-469
1330	LIM	LIM domain	4.6	-17.3	1	461-525
1330	zf-MYND	MYND finger	8.4	-12.1	1	405-453
1331	SCAN	SCAN domain	1.3e-57	204.8	1	31-123
1331	KRAB	KRAB box	0.038	12.6	1	218-251
1332	MyTH4	MyTH4 domain	1.4e-19	78.5	1	769-887
1332	RhoGAP	RhoGAP domain	7.3e-19	76.1	1	917-1064
1332	WW	WW domain	0.00061	26.5	2	26-56:65-95
1333	EPTP	EPTP domain	1.5e-50	181.4	2	204-335:386-518
1333	LRRCT	Leucine rich repeat C-terminal domain	4.8e-10	46.8	1	147-196
1333	LRR	Leucine Rich Repeat	9.4e-06	32.5	2	68-91:92-115
1334	SART-1	SART-1 family	6.4	-358.3	1	42-710
1337	DnaJ	DnaJ domain	3.4e-18	73.9	1	11-82
1338	dsrm	Double-stranded RNA binding motif	8.8	-9.3	1	30-103
1339	Ubie_methyltran	ubiE/COQ5 methyltransferase family	0.21	-144.6	1	24-200
1339	CheR	CheR methyltransferase, SAM binding d	7.8	-114.0	1	40-163
1344	zf-C2H2	Zinc finger, C2H2 type	1.8e-71	250.9	9	144-166:172-194:200-222:228-250:256-278:284-

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Table 4B

						306:312- 334:340- 362:368-390
1344	FYVE	FYVE zinc finger	2.6	-20.5	1	306-379
1344	zf-BED	BED zinc finger	3.1	-2.8	2	245-279:325- 363
1344	zf-UBR1	Putative zinc finger in N- recognin	3.6	-20.4	1	259-333
1349	zf-C2H2	Zinc finger, C2H2 type	2.3e-50	180.8	7	251-273:279- 301:307- 329:335- 357:363- 385:391- 413:419-441
1349	KRAB	KRAB box	6.4e-24	92.9	1	48-88
1349	zf-CCHC	Zinc knuckle	1.5	6.3	1	251-268
1349	zf-BED	BED zinc finger	2	-1.2	1	376-414
1350	rvp	Retroviral aspartyl protease	0.012	-0.6	1	126-246
1351	SH3	SH3 domain	8.7e-18	72.5	1	287-341
1351	DAG_PE- bind	Phorbol esters/diacylglycerol binding dom	8.7e-05	27.4	1	103-153
1351	DC1	DC1 domain	0.66	11.2	1	114-145
1352	adenylatekin ase	Adenylate kinase	7.1e-36	132.6	1	54-211
1352	Thymidylate kin	Thymidylate kinase	0.69	-50.9	1	54-228
1352	IPT	Isopentenyl transferase	4.8	-157.5	1	49-246
1352	AAA	ATPase family associated with various	6.6	-44.9	1	51-253
1354	COX6B	Cytochrome oxidase c subunit VIb	1e-32	122.1	1	10-87
1356	Ribosomal_ L37e	Ribosomal protein L37e	3.2e-31	117.1	1	2-55
1358	Troponin	Troponin	3.2e-37	137.1	1	133-275
1359	spectrin	Spectrin repeat	1	-9.4	1	136-245
1359	filament	Intermediate filament protein	5.4	-203.8	1	4-246
1359	bZIP_Maf	bZIP Maf transcription factor	7	-78.0	1	155-262
1360	Glyco_trans f_10	Glycosyltransferase family 10	2.5e-07	-22.5	1	70-455
1361	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.9e-06	34.9	1	228-265
1361	LON	ATP-dependent protease La (LON) domain	1.3e-05	26.8	1	309-514
1361	OAR	OAR domain	3.4	5.1	1	100-119
1361	TPR	TPR Domain	7.3	7.4	1	44-77
1362	rvt	Reverse transcriptase	7e-30	112.7	1	210-392
1362	rnaseH	RNase H	2.8e-20	80.8	1	646-788
1362	rvp	Retroviral aspartyl protease	7.1e-18	72.8	1	39-136
1362	zf-CCHC	Zinc knuckle	0.014	19.6	1	24-41
1363	DUF232	Putative transcriptional regulator	1.8	-21.3	1	493-622
1363	Borrelia_orf A	Borrelia ORF-A	2.3	-85.6	1	340-636
1363	filament	Intermediate filament protein	3.7	-199.4	1	359-681
1363	Mlp	Mlp lipoprotein family	3.9	-31.5	1	456-679
1363	PFEMP	Plasmodium falciparum erythrocyte mem	4.4	-83.2	1	141-255

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Table 4B

1363	Phe_tRNA-synt_N	Aminoacyl tRNA synthetase class II, N	7.3	-24.8	1	53-116
1364	KRAB	KRAB box	1.1e-26	102.1	1	27-67
1366	Tymo_45kd_70kd	Tymovirus 45/70Kd protein	3.1	-290.1	1	149-526
1367	zf-C2H2	Zinc finger, C2H2 type	1.7e-126	433.6	17	349-371:377-399:405-427:433-455:461-483:489-511:517-539:545-566:572-594:600-622:628-650:656-678:684-706:712-734:740-762:768-790:796-818
1367	KRAB	KRAB box	2.3e-21	84.4	1	34-74
1367	zf-BED	BED zinc finger	1.7	-0.6	1	669-707
1367	LIM	LIM domain	4.1	-16.8	1	407-459
1370	bromodomain	Bromodomain	3.2e-29	110.5	1	107-193
1370	Tymo_45kd_70kd	Tymovirus 45/70Kd protein	9.9	-304.3	1	346-685
1371	Peptidase_M1	Peptidase family M1	7.9e-100	345.1	1	40-425
1371	Sigma70_ECF	Sigma-70 factor (ECF subfamily)	1.1	-8.4	1	430-470
1372	rrm	RNA recognition motif.	1.7e-21	84.8	1	354-425
1374	Tymo_45kd_70kd	Tymovirus 45/70Kd protein	5.3	-296.7	1	38-427
1375	filament	Intermediate filament protein	0.86	-183.1	1	41-302
1375	Tektin	Tektin family	4.8	-238.0	1	9-305
1376	zf-C2H2	Zinc finger, C2H2 type	1.4e-111	384.1	13	138-160:166-188:194-216:222-244:250-272:278-300:306-328:334-356:362-384:390-412:418-440:446-468:474-496
1376	zf-BED	BED zinc finger	1.5	0.1	1	459-497
1376	TFIIS	Transcription factor S-II (TFIIS)	3.4	-3.2	1	309-344
1376	PHD	PHD-finger	4.5	-15.9	1	195-258
1376	LIM	LIM domain	4.9	-17.5	1	364-428
1377	HMG_box	HMG (high mobility group) box	2.8e-06	34.3	1	42-110
1377	zf-	Topoisomerase DNA binding	5.9	-4.0	1	639-664

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Table 4B

	C4_Topoiso m	C4 zinc fing				
1377	Tymo_45kd 70kd	Tymovirus 45/70Kd protein	7.1	-300.3	1	268-669
1380	Mtap_PNP	Phosphorylase family 2	2e-159	543.0	1	9-286
1386	zf-C2H2	Zinc finger, C2H2 type	1.6e-18	75.0	12	169-195:212- 241:253- 277:315- 337:362- 386:498- 521:531- 554:606- 631:636- 659:667- 689:753- 776:789-812
1386	PHD	PHD-finger	3.7	-15.2	1	607-644
1386	UIM	Ubiquitin interaction motif	7.5	10.8	1	1044-1061
1386	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	9.5	-8.2	1	608-641
1387	F-box	F-box domain	0.00022	28.0	1	59-106
1389	zf-C2H2	Zinc finger, C2H2 type	1.1e-116	401.1	16	92-114:120- 142:148- 170:176- 198:204- 226:232- 254:260- 282:288- 310:316- 338:344- 366:372- 394:400- 422:428- 450:456- 478:504- 526:532-553
1389	LIM	LIM domain	1.5	-13.2	1	290-354
1389	zf-BED	BED zinc finger	4.6	-4.4	1	189-227
1389	TFIIS	Transcription factor S-II (TFIIS)	4.9	-4.5	1	232-270
1390	MMTV_SA g	Mouse mammary tumor virus superantigen	8.2	-118.1	1	119-388
1391	kinesin	Kinesin motor domain	1.4e-82	287.8	1	1-238
1394	Mov34	Mov34/MPN/PAD-1 family	6.2e-28	106.2	1	50-162
1395	T-box	T-box	4.7e-128	438.8	1	114-305
1397	zf-C2H2	Zinc finger, C2H2 type	1.2e-113	391.0	15	48-70:197- 219:225- 247:253- 275:281- 303:309- 331:337- 359:365- 387:393- 415:421- 443:449- 471:477- 499:505-

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Table 4B

						527:533- 555:561-583
1397	zf-MIZ	MIZ zinc finger	3.5	-17.8	1	238-292
1397	LIM	LIM domain	5.1	-17.7	1	311-365
1397	TFIIS	Transcription factor S-II (TFIIS)	5.6	-5.0	1	424-459
1397	zf-BED	BED zinc finger	8	-6.5	2	462-500:508- 556
1397	PHD	PHD-finger	9	-18.7	1	310-373
1397	DM-domain	DM DNA binding domain	9.3	-13.0	1	503-551
1398	WD40	WD domain, G-beta repeat	1.6e-27	104.8	7	188-224:231- 269:278- 315:326- 363:382- 418:429- 466:473-509
1400	Dynein_heavy	Dynein heavy chain	9.5e-237	799.9	1	442-1141
1400	VHS	VHS domain	8.3	-54.3	1	535-656
1401	Ribosomal_L11	Ribosomal protein L11	1.7e-53	191.2	1	13-134
1403	PWWP	PWWP domain	3.1e-10	47.4	1	352-428
1404	zf-C2H2	Zinc finger, C2H2 type	1.2e-205	696.5	27	126-148:154- 176:182- 204:210- 232:238- 260:266- 288:294- 316:322- 344:350- 372:378- 400:406- 428:434- 456:462- 484:490- 512:518- 540:546- 568:574- 596:602- 624:630- 652:658- 680:686- 708:714- 736:742- 764:770- 792:798- 820:826- 848:854-876
1404	GATA	GATA zinc finger	0.9	-4.3	1	488-534
1404	zf-UBR1	Putative zinc finger in N- recognin	1.4	-16.4	1	589-651
1404	zf-MIZ	MIZ zinc finger	2.8	-17.1	1	643-697
1404	PHD	PHD-finger	3.7	-15.1	1	155-190
1404	LIM	LIM domain	4.4	-17.2	1	408-472
1404	DnaJ_CXX CXGXXG	DnaJ central domain (4 repeats)	7.9	-49.7	1	440-503
1408	FYVE	FYVE zinc finger	1.5e-28	108.3	2	150-217:267-

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Table 4B

						333
1408	zf-AN1	AN1-like Zinc finger	0.68	-0.7	1	278-313
1411	K-box	K-box region	4.4	-38.7	1	360-445
1415	FYVE	FYVE zinc finger	8.2e-12	52.7	1	39-105
1416	BAD	Bacterial transcriptional activator domain	1.4	-69.0	1	678-793
1416	Gag_p24	gag gene protein p24	3.3	-78.4	1	613-810
1417	CH	Calponin homology (CH) domain	5.7e-16	66.5	1	965-1070
1418	PH	PH domain	5.3e-21	83.2	1	6-117
1419	PH	PH domain	5.3e-21	83.2	1	6-117
1420	pkinase	Protein kinase domain	1.9e-14	61.4	1	116-508
1423	PA28_beta	Proteasome activator pa28 beta subunit	5.2e-117	402.1	1	105-254
1423	PA28_alpha	Proteasome activator pa28 alpha subunit	1.8e-43	157.8	1	7-70
1424	PAE	Pectinacetylase	0.0051	-196.0	1	1-280
1425	NDK	Nucleoside diphosphate kinase	2.8e-08	-9.8	1	157-312
1425	thioredo	Thioredoxin	0.0051	-7.1	1	9-114
1427	K_tetra	K ⁺ channel tetramerisation domain	2.4e-15	64.4	1	26-133
1430	ank	Ankyrin repeat	2.3e-63	224.0	8	11-44:45-77:78-110:111-143:144-176:177-209:210-240:242-274
1431	HLH	Helix-loop-helix DNA-binding domain	3.5e-11	50.6	1	113-165
1434	zf-C2H2	Zinc finger, C2H2 type	1e-190	647.0	24	276-298:304-326:332-354:360-382:388-410:416-438:444-466:472-494:500-522:528-550:556-578:584-606:612-634:640-662:668-690:696-718:724-746:752-774:780-802:808-830:836-858:864-886:892-914:920-942
1434	KRAB	KRAB box	6.5e-25	96.2	1	81-121
1434	TFIIS	Transcription factor S-II (TFIIS)	0.96	1.5	1	500-538
1434	S_mold_rep	Dictyostelium (slime mold)	1	12.8	3	307-330:531-

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Table 4B

	eat	repeat				554:923-946
1434	LIM	LIM domain	2.8	-15.4	1	558-622
1434	E6	Early Protein (E6)	4.3	-65.3	1	642-729
1434	ZZ	Zinc finger, ZZ type	7.7	-4.0	1	804-851
1435	Collagen	Collagen triple helix repeat (20 copies)	7.2	-65.6	1	392-450
1437	Ribosomal_L29	Ribosomal L29 protein	1.3e-14	62.0	1	6-69
1439	zf-C2H2	Zinc finger, C2H2 type	6.9e-88	305.4	11	170-192:198-220:226-248:254-276:282-304:310-332:338-360:366-388:394-416:422-444:450-472
1439	KRAB	KRAB box	5.6e-25	96.4	1	6-46
1439	TFIIS	Transcription factor S-II (TFIIS)	5.8	-5.1	1	397-432
1439	zf-UBR1	Putative zinc finger in N-recognin	6	-22.6	1	173-241
1439	LIM	LIM domain	9.2	-19.8	1	368-432
1440	rrm	RNA recognition motif.	0.087	13.2	1	17-91
1444	Paxillin	Paxillin family	5.9	-111.7	1	612-799
1446	zf-C2H2	Zinc finger, C2H2 type	2.2e-100	346.9	14	27-49:55-77:83-105:111-130:136-158:164-186:192-214:220-242:248-270:276-298:304-326:332-354:360-382:388-410
1446	FYVE	FYVE zinc finger	1.2	-17.3	1	298-371
1446	LIM	LIM domain	2.2	-14.6	1	166-230
1446	Yippee	Yippee putative zinc-binding protein	2.8	-64.6	1	126-188
1446	zf-BED	BED zinc finger	3.5	-3.3	1	293-327
1446	PHD	PHD-finger	4.8	-16.1	1	137-200
1447	K-box	K-box region	0.24	-23.3	1	64-154
1448	K-box	K-box region	0.24	-23.3	1	64-154
1450	spidertoxin	Spider toxin	4.4	-5.1	1	243-275
1451	zf-C2H2	Zinc finger, C2H2 type	7e-115	395.1	16	156-178:184-206:212-234:240-262:268-290:296-318:324-346:352-374:380-402:408-

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Table 4B

						430:436- 458:464- 486:492- 514:520- 542:548- 570:576-598
1451	TFIIS	Transcription factor S-II (TFIIS)	2.4	-1.9	1	324-362
1451	LIM	LIM domain	6.6	-18.6	1	242-306
1451	zf-TRAF	TRAF-type zinc finger	7.2	-8.3	1	262-311
1454	zf-C2H2	Zinc finger, C2H2 type	1.9e-157	536.4	19	139-161:167- 189:195- 217:223- 245:251- 273:279- 301:307- 329:335- 357:363- 385:391- 413:419- 441:447- 469:475- 497:503- 525:531- 553:559- 581:587- 609:615- 637:643-665
1454	KRAB	KRAB box	1.3e-27	105.2	1	6-46
1454	LIM	LIM domain	2.2	-14.5	1	337-401
1454	zf-BED	BED zinc finger	3.4	-3.2	1	432-470
1455	zf-C2H2	Zinc finger, C2H2 type	1.8e-37	137.9	6	57-79:85- 107:113- 136:283- 305:311- 333:398-420
1455	GATA	GATA zinc finger	3.1	-8.4	1	281-327
1455	PHD	PHD-finger	3.3	-14.7	1	399-434
1455	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.3	-6.0	1	285-316
1457	SCAN	SCAN domain	3e-61	216.9	1	26-121
1457	zf-C2H2	Zinc finger, C2H2 type	6.8e-49	175.9	6	692-714:720- 742:748- 770:776- 798:804- 826:832-854
1457	zf-BED	BED zinc finger	1.2	0.9	1	705-743
1457	TFIIS	Transcription factor S-II (TFIIS)	3.2	-2.9	1	751-786
1458	pKID	pKID domain	4.6e-24	93.4	1	51-92
1459	LRR	Leucine Rich Repeat	0.0001	29.1	4	87-110:145- 172:173- 196:201-224
1460	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	0.0011	25.7	1	295-321
1462	ABC1	ABC1 family	1.3e-41	151.7	1	180-296
1462	MeMO_Hy	Methane monooxygenase,	4.6	-98.8	1	173-336

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Table 4B

	d_G	hydrolase gamma cha				
1463	Pur_DNA_glyco	Methylpurine-DNA glycosylase (MPG)	6.5e-118	405.1	1	70-267
1464	Pur_DNA_glyco	Methylpurine-DNA glycosylase (MPG)	1.7e-120	413.7	1	217-414
1465	Troponin	Troponin	2.4e-20	81.0	1	792-997
1465	IQ	IQ calmodulin-binding motif	4.1	13.8	1	269-289
1466	CUB	CUB domain	1.6e-84	294.2	3	128-233:305-410:477-582
1466	sushi	Sushi domain (SCR repeat)	5.7e-31	116.3	3	67-124:244-301:418-473
1466	DUF141	Domain of unknown function DUF141	8	-16.0	1	123-237
1468	FHA	FHA domain	5.4	-3.7	1	64-127
1469	Tropomyosin	Tropomyosin	2.1	-109.1	1	467-690
1469	TBC	TBC domain	2.8	-97.3	1	271-500
1470	trypsin	Trypsin	0.19	-38.0	1	3-96
1471	trypsin	Trypsin	2.5e-83	290.2	1	64-291
1472	dynamamin	Dynamamin family	6.6	-83.3	1	397-577
1474	DEAD	DEAD/DEAH box helicase	8.6	-78.2	1	567-732
1475	DEAD	DEAD/DEAH box helicase	8.6	-78.2	1	524-689
1478	zf-C2H2	Zinc finger, C2H2 type	2.5e-26	100.9	5	357-382:388-412:418-440:446-468:476-499
1478	zf-BED	BED zinc finger	1.1	1.2	1	372-413
1480	zf-C2H2	Zinc finger, C2H2 type	1.7e-29	111.4	7	53-76:237-261:279-301:374-396:402-426:432-454:469-493
1480	PHD	PHD-finger	0.8	-9.0	1	433-477
1480	zf-BED	BED zinc finger	9.7	-7.3	1	270-302
1482	Spin-Ssty	Spin/Ssty Family	0.28	10.8	1	50-77
1488	zf-C2H2	Zinc finger, C2H2 type	2.5e-23	90.9	3	296-320:326-350:356-378
1488	TT_ORF2	TT viral ORF2	8.3	-97.5	1	125-231
1489	Ets	Ets-domain	4.3e-36	133.3	1	110-196
1493	TTL	Tubulin-tyrosine ligase family	7.2e-16	66.1	1	1-272
1495	zf-CCHC	Zinc knuckle	0.22	11.7	1	106-125
1495	zf-A20	A20-like zinc finger	6.2	4.0	1	105-129
1496	DnaJ	DnaJ domain	6.6e-40	146.0	1	3-69
1497	homeobox	Homeobox domain	1e-20	82.3	1	243-294
1501	homeobox	Homeobox domain	4.1e-31	116.8	1	83-139
1507	Kelch	Kelch motif	4.9e-56	199.6	6	305-352:354-406:408-453:455-500:502-552:554-601
1507	BTB	BTB/POZ domain	8.2e-21	82.6	1	63-167
1508	homeobox	Homeobox domain	5.6e-24	93.1	1	19-73
1510	TF_AP-2	Transcription factor AP-2	4.5e-130	445.5	1	52-259
1512	MIF4G	MIF4G domain	4.8e-37	136.5	1	163-346
1512	MA3	MA3 domain	1.9e-25	98.0	1	455-561

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1512	UPF0050	Domain of unknown function DUF	1.9	-44.5	1	222-324
1512	zf-TAZ	TAZ zinc finger	2	-27.2	1	227-285
1512	RYDR_ITP R	RIH domain	5	-48.0	1	141-343
1512	NB-ARC	NB-ARC domain	5.7	-147.7	1	139-381
1513	zf-AN1	AN1-like Zinc finger	1.5e-18	75.1	1	667-708
1513	ubiquitin	Ubiquitin family	4.3e-18	73.5	1	28-101
1514	SET	SET domain	2.9e-63	223.6	1	1596-1725
1514	PHD	PHD-finger	5.6e-32	119.7	3	1206- 1250:1370- 1412:1781- 1828
1514	PWWP	PWWP domain	1.9e-31	117.9	1	1414-1490
1514	zf-AN1	AN1-like Zinc finger	4.3	-7.2	1	1825-1859
1514	Furin-like	Furin-like cysteine rich region	9.2	-98.4	1	1204-1344
1518	F-protein	Negative factor, (F-Protein) or Nef	4.9	-106.1	1	123-287
1519	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.55	2.6	1	916-953
1521	Exonuc_VII L	Exonuclease VII, large subunit	7.1	-86.7	1	231-381
1525	MAGE	MAGE family	8.5e-05	-71.1	1	2-170
1526	FAD_bindin g_6	Oxidoreductase FAD-binding domain	6.4e-25	96.2	1	79-176
1526	NAD_bindi ng	Oxidoreductase NAD-binding domain	3.9e-05	24.6	1	181-298
1527	DENN	DENN (AEX-3) domain	3.2e-83	289.9	1	90-293
1527	uDENN	uDENN domain	6.7e-27	102.8	1	1-89
1527	dDENN	dDENN domain	2.6e-22	87.5	1	324-391
1528	DENN	DENN (AEX-3) domain	3.2e-83	289.9	1	172-375
1528	uDENN	uDENN domain	4.8e-23	90.0	1	85-171
1528	dDENN	dDENN domain	2.6e-22	87.5	1	406-473
1529	ERM	Ezrin/radixin/moesin family	5.7	-218.2	1	272-528
1530	rvt	Reverse transcriptase	6.7	-58.1	1	1-118
1531	myb_DNA- binding	Myb-like DNA-binding domain	6.9e-21	82.8	2	88-133:285- 330
1531	ELM2	ELM2 domain	8.4e-16	65.9	1	2-63
1532	zf-C2H2	Zinc finger, C2H2 type	5.2e-15	63.3	8	241-264:290- 314:320- 342:603- 626:709- 732:843- 866:880- 903:1000- 1023
1533	Flotillin	Flotillin family	2.2e-107	370.2	1	193-366
1533	Band_7	SPFH domain / Band 7 family	1.9e-38	141.1	1	3-188
1533	vATP- synt_E	ATP synthase (E/31 kDa) subunit	5.9	-94.9	1	251-400
1534	PH	PH domain	2.7e-52	187.1	5	88-179:201- 289:504- 610:629- 714:1035- 1156
1534	RhoGAP	RhoGAP domain	2.6e-41	150.7	1	731-881
1534	ArfGap	Putative GTP-ase activating	1.1e-27	105.5	1	295-419

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Table 4B

		protein for Arf				
1534	RA	Ras association (RalGDS/AF-6) domain	0.15	0.7	1	932-1021
1534	Pox_B15	B15-like protein	9.5	-65.1	1	728-850
1534	Relaxase	Relaxase/Mobilization nuclease domain	9.7	-79.3	1	757-999
1535	PH	PH domain	1.5e-52	188.0	5	88-179:201-289:504-610:629-714:1035-1145
1535	RhoGAP	RhoGAP domain	2.6e-41	150.7	1	731-881
1535	ArfGap	Putative GTP-ase activating protein for Arf	1.1e-27	105.5	1	295-419
1535	RA	Ras association (RalGDS/AF-6) domain	0.15	0.7	1	932-1021
1535	Pox_B15	B15-like protein	9.5	-65.1	1	728-850
1535	Relaxase	Relaxase/Mobilization nuclease domain	9.7	-79.3	1	757-999
1536	SH3	SH3 domain	0.00013	27.4	1	15-72
1537	TF_Otx	Otx1 transcription factor	8.9	-35.4	1	234-302
1537	Herpes_LP	Herpesvirus leader protein	9.9	-89.9	1	111-246
1538	UPF0131	Uncharacterised protein family (UPF0131)	5.4e-12	53.3	1	11-140
1540	Ndr	Ndr family	6.7e-84	292.1	1	32-228
1540	abhydrolase	alpha/beta hydrolase fold	4.6	-19.5	1	5-221
1541	Ribosomal_L35p	Ribosomal protein L35	6e-26	99.6	1	4-62
1542	PHD	PHD-finger	0.12	-1.3	1	81-131
1543	RA	Ras association (RalGDS/AF-6) domain	8.4	-16.1	1	124-214
1546	TPR	TPR Domain	0.0067	23.1	2	134-167:203-236
1547	ARID	ARID/BRIGHT DNA binding domain	2.1e-43	157.6	1	603-712
1548	Kelch	Kelch motif	3.7e-41	150.2	5	20-66:68-114:116-162:164-209:211-260
1552	GST_N	Glutathione S-transferase, N-terminal domain	2.7e-10	47.6	1	3-82
1552	GST_C	Glutathione S-transferase, C-terminal domain	0.22	7.3	1	47-155
1554	GTP_EFTU_D2	Elongation factor Tu domain 2	5.9e-07	36.5	1	65-148
1554	GTP_EFTU_D3	Elongation factor Tu C-terminal domain	8.1e-07	33.1	1	153-243
1555	rrm	RNA recognition motif.	0.055	15.3	1	45-115
1556	pkinase	Protein kinase domain	8.4e-38	139.0	1	8-265
1557	pkinase	Protein kinase domain	4e-41	150.1	1	8-265
1559	5-FTHF_cyc-lig	5-formyltetrahydrofolate cyclo-ligase	1.8e-21	84.7	1	8-207
1559	rrm	RNA recognition motif.	3e-06	34.2	1	308-374
1561	zf-UBR1	Putative zinc finger in N-recogin	6.6	-23.0	1	121-173
1562	ig	Immunoglobulin domain	8.5e-07	36.0	1	87-146

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Table 4B

1563	RasGEF	RasGEF domain	1.7e-88	307.4	1	1311-1496
1563	RhoGEF	RhoGEF domain	8.2e-68	238.7	1	559-740
1563	PH	PH domain	1.3e-34	128.4	2	335-445:772-900
1563	RasGEFN	Guanine nucleotide exchange factor for Ras-l	4.9e-18	73.3	1	945-1000
1563	IQ	IQ calmodulin-binding motif	0.012	22.2	1	518-538
1564	RasGEF	RasGEF domain	1.7e-88	307.4	1	999-1184
1564	RhoGEF	RhoGEF domain	8.2e-68	238.7	1	247-428
1564	PH	PH domain	1.3e-34	128.4	2	23-133:460-588
1564	RasGEFN	Guanine nucleotide exchange factor for Ras-l	4.9e-18	73.3	1	633-688
1564	IQ	IQ calmodulin-binding motif	0.012	22.2	1	206-226
1569	ferritin	Ferritin-like domain	9.6e-94	324.8	2	56-197:199-317
1570	CUB	CUB domain	2e-57	204.2	2	107-212:279-383
1570	sushi	Sushi domain (SCR repeat)	3.6e-25	97.1	2	48-103:220-275
1570	DUF141	Domain of unknown function DUF141	3.8	-12.4	1	102-216
1571	Kelch	Kelch motif	1.5e-10	48.5	2	349-398:401-446
1571	BTB	BTB/POZ domain	0.026	8.5	1	93-207
1572	MBD	Methyl-CpG binding domain	0.089	11.8	1	17-61
1573	ubiquitin	Ubiquitin family	2.5e-15	64.3	1	1-72
1574	OTU	OTU-like cysteine protease	0.73	-9.5	1	166-283
1574	Bcl-2	Apoptosis regulator proteins, Bcl-2 family	9.7	-29.5	1	135-203
1575	UPF0148	Uncharacterised protein family (UPF0148)	5.8	-33.4	1	43-165
1576	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0027	22.5	1	357-395
1577	ArfGap	Putative GTP-ase activating protein for Arf	9.7e-47	168.7	1	11-127
1579	filament	Intermediate filament protein	1.4e-128	440.6	1	85-400
1579	ubiquitin	Ubiquitin family	6.6	-5.3	1	316-394
1579	RecT	RecT protein	6.8	-123.5	1	288-430
1579	RasGAP_C	RasGAP C-terminus	8.6	-35.0	1	305-447
1579	spectrin	Spectrin repeat	9	-20.3	1	267-375
1581	lactamase_B	Metallo-beta-lactamase superfamily	0.17	-10.7	1	25-182
1582	Keratin_B2	Keratin, high sulfur B2 protein	1.6e-06	22.3	1	5-154
1583	ParA	ParA family ATPase	0.009	5.5	1	105-211
1583	ArsA_ATPase	Anion-transporting ATPase	5.2	-192.3	1	55-251
1585	crystall	Beta/Gamma crystallin	3.3e-73	256.6	4	15-101:109-190:203-282:290-370
1585	Ricin_B_lectin	QXW lectin repeat	0.0012	25.6	2	420-462:463-507
1587	T-box	T-box	9.9e-75	261.7	1	1-149
1589	LRR	Leucine Rich Repeat	1e-10	49.1	9	115-139:171-195:199-226:227-251:255-

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Table 4B

						278:283- 307:339- 363:367- 390:397-421
1590	60s_ribosomal	60s Acidic ribosomal protein	8.6e-33	122.4	1	1-100
1591	FMO-like	Flavin-binding monooxygenase-like	0	1158.7	1	49-598
1591	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	0.0037	-35.7	1	51-424
1592	FMO-like	Flavin-binding monooxygenase-like	0	1158.7	1	87-636
1592	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	0.0037	-35.7	1	89-462
1593	Nucleoplasmin	Nucleoplasmin	3	-91.3	1	257-414
1594	LIM	LIM domain	7.3e-45	162.5	2	27-86:89-148
1594	homeobox	Homeobox domain	5e-16	66.7	1	192-248
1597	LRR	Leucine Rich Repeat	0.0064	23.1	4	161-184:189- 213:217- 240:245-272
1600	bromodomain	Bromodomain	4.6e-182	618.2	6	50-139:186- 275:386- 475:523- 613:662- 751:782-867
1600	BAH	BAH domain	2.3e-65	230.6	2	956- 1049:1131- 1247
1600	HMG_box	HMG (high mobility group) box	2.1e-07	38.0	1	1328-1384
1601	Armadillo_seg	Armadillo/beta-catenin-like repeat	3.8e-08	40.5	4	20-61:62- 103:106- 146:147-193
1601	BTB	BTB/POZ domain	0.23	-3.1	1	571-695
1604	zf-C2H2	Zinc finger, C2H2 type	3.8e-83	289.6	13	123-146:151- 170:270- 292:298- 320:326- 348:354- 376:382- 404:410- 432:438- 460:466- 488:494- 516:522- 544:550-572
1604	KRAB	KRAB box	4.1e-21	83.6	1	46-86
1604	zf-BED	BED zinc finger	0.53	4.0	2	248-293:479- 517
1604	LIM	LIM domain	1.7	-13.7	1	440-494
1604	zf-TRAF	TRAF-type zinc finger	2.9	-4.0	1	488-539
1604	PHD	PHD-finger	8.9	-18.7	1	467-530
1606	TIR	TIR domain	2.5	-29.3	1	81-209
1609	Gelsolin	Gelsolin repeat	2.1e-48	174.3	5	522-574:645- 685:778- 818:1088-

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Table 4B

						1135:1197-1238
1609	LRR	Leucine Rich Repeat	7.7e-45	162.4	14	9-33:34-56:57-79:120-142:143-166:167-189:190-213:214-238:239-261:262-284:285-307:308-332:333-355:356-378
1611	zf-C2H2	Zinc finger, C2H2 type	4.8e-09	43.5	3	44-66:72-94:100-124
1611	LIM	LIM domain	6.1	-18.3	1	74-136
1611	PHD	PHD-finger	6.3	-17.3	1	73-108
1612	filament	Intermediate filament protein	1.1	-185.9	1	209-509
1612	RNA_pol_A_CTD	Bacterial RNA polymerase, alpha chain C	3.6	-26.3	1	301-359
1612	DUF232	Putative transcriptional regulator	5.8	-27.4	1	481-606
1612	Borrelia_orf A	Borrelia ORF-A	8	-100.4	1	266-641
1612	GM_CSF	Granulocyte-macrophage colony-stimulati	9	-10.7	1	264-381
1612	DUF38	Domain of unknown function DUF38	9.7	-42.7	1	45-165
1613	AUX_IAA	AUX/IAA family	1.7	-123.7	1	367-548
1613	RNA_pol_A_CTD	Bacterial RNA polymerase, alpha chain C	3.6	-26.3	1	301-359
1613	GM_CSF	Granulocyte-macrophage colony-stimulati	9	-10.7	1	264-381
1613	Borrelia_orf A	Borrelia ORF-A	9.1	-102.1	1	266-588
1613	DUF38	Domain of unknown function DUF38	9.7	-42.7	1	45-165
1613	DNA_topois oIV	DNA gyrase/topoisomerase IV, subunit A	9.9	-368.9	1	187-538
1614	Amino_oxidase	Flavin containing amine oxidoreductase	0.03	-46.6	1	46-434
1614	pyr_redox	Pyridine nucleotide-disulphide oxidored	6.8	-93.2	1	36-370
1615	PAP_assoc	PAP/25A associated domain	1.3e-41	151.7	2	188-241:833-886
1615	zf-CCHC	Zinc knuckle	2.1e-18	74.6	3	601-618:945-962:1051-1068
1615	NTP_transf_2	Nucleotidyltransferase domain	0.011	21.7	1	660-752
1619	zf-AN1	AN1-like Zinc finger	0.00034	26.1	2	10-52:64-106
1620	zf-AN1	AN1-like Zinc finger	0.087	6.5	1	51-93
1621	Tropomodulin	Tropomodulin	0.94	-150.3	1	95-373
1622	kinesin	Kinesin motor domain	1.2e-146	500.6	1	68-358

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Table 4B

1622	ALA_synthase	Aminolevulinic acid synthase domain	9.8	-34.1	1	153-204
1623	WD40	WD domain, G-beta repeat	5e-46	166.3	12	103-141:147-185:191-225:287-321:351-387:396-441:484-520:565-604:611-648:659-695:704-740:778-812
1624	bromodomain	Bromodomain	6.5e-13	56.3	1	50-137
1625	zf-C2H2	Zinc finger, C2H2 type	5.5e-35	129.6	6	150-173:356-378:384-406:725-747:753-775:783-806
1625	PHD	PHD-finger	4.1	-15.5	1	726-791
1625	zf-BED	BED zinc finger	4.8	-4.5	1	766-807
1626	TUDOR	Tudor domain	1.1e-64	228.4	2	653-780:913-1031
1627	PWI	PWI domain	1.2e-35	131.8	1	8-79
1631	zf-C2H2	Zinc finger, C2H2 type	1.7e-59	211.1	9	149-169:177-199:205-227:233-255:261-283:289-311:317-339:345-367:373-395
1631	KRAB	KRAB box	9.4e-23	89.0	1	29-69
1631	TFIIS	Transcription factor S-II (TFIIS)	1.6	-0.3	2	177-215:261-299
1631	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	8.9	-7.9	1	151-182
1634	2OG-FeII_Oxy	2OG-Fe(II) oxygenase superfamily	0.0071	20.3	1	155-249
1637	T-box	T-box	2.1e-77	270.6	1	1-164
1640	homeobox	Homeobox domain	1.5e-26	101.7	1	118-174
1645	homeobox	Homeobox domain	1.1e-34	128.6	2	16-75:102-158
1646	Keratin_B2	Keratin, high sulfur B2 protein	0.00047	-16.3	2	16-164:169-321
1647	BAD	Bacterial transcriptional activator domain	6.3	-77.5	1	19-138
1649	HMG_box	HMG (high mobility group) box	5.4e-20	79.8	1	100-168
1651	zf-C2H2	Zinc finger, C2H2 type	1.8e-27	104.7	6	65-87:101-123:129-151:196-218:224-246:252-274
1651	LIM	LIM domain	4.1	-16.9	1	226-280
1652	zf-C2H2	Zinc finger, C2H2 type	4.7e-165	561.7	21	216-240:274-

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Table 4B

						296:352- 374:380- 402:408- 430:436- 458:464- 486:492- 514:520- 542:548- 570:576- 598:604- 626:632- 654:660- 682:688- 710:716- 738:744- 766:772- 794:800- 822:828- 850:856-879
1652	GATA	GATA zinc finger	2.4	-7.5	1	742-788
1652	zf-BED	BED zinc finger	2.5	-2.0	2	421-459:757- 795
1652	S_mold_rep eat	Dictyostelium (slime mold) repeat	2.9	10.9	7	162-185:190- 213:249- 272:277- 300:663- 686:775- 798:831-854
1652	LIM	LIM domain	3.2	-16.0	1	718-777
1652	zf-MIZ	MIZ zinc finger	3.5	-17.8	1	591-643
1652	TFIIS	Transcription factor S-II (TFIIS)	3.8	-3.6	1	716-754
1656	MAGE	MAGE family	5.9e-22	86.4	1	36-288
1660	Ribosomal_ L15	Ribosomal protein L15 amino terminal re	9.7	-48.3	1	970-1050
1661	zf-C2H2	Zinc finger, C2H2 type	4.2e-89	309.4	12	193-215:221- 243:249- 271:277- 299:305- 327:333- 355:361- 383:389- 411:417- 439:445- 467:501- 523:529-554
1661	TFIIS	Transcription factor S-II (TFIIS)	0.21	7.0	1	221-259
1661	zf-TRAF	TRAF-type zinc finger	4.6	-6.3	1	295-348
1665	homeobox	Homeobox domain	2.6e-28	107.5	1	164-220
1665	Collagen	Collagen triple helix repeat (20 copies)	9.6	-68.0	1	213-271
1666	Transposase 8	Transposase	5	-15.4	1	1035-1112
1666	Ribosomal_ L29	Ribosomal L29 protein	7.6	-14.5	1	1070-1113
1667	Transposase	Transposase	5	-15.4	1	1015-1092

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Table 4B

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1667	Ribosomal_L29	Ribosomal L29 protein	7.6	-14.5	1	1050-1093
1670	SAP	SAP domain	2.1	8.3	1	92-126
1671	zf-C2H2	Zinc finger, C2H2 type	6.6e-29	109.5	6	400-424:432-455:461-483:489-511:517-540:546-568
1671	SET	SET domain	0.0031	-23.0	1	246-373
1671	zf-BED	BED zinc finger	1.7	-0.6	1	530-569
1671	zf-TRAF	TRAF-type zinc finger	2.8	-3.8	1	455-504
1671	zf-AN1	AN1-like Zinc finger	3.2	-6.2	1	491-545
1674	PHD	PHD-finger	1.7e-10	48.3	1	312-357
1678	RNase_PH	3' exoribonuclease family, domain 1	1.6e-45	164.7	1	31-166
1678	RNase_PH_C	3' exoribonuclease family, domain 2	4.4e-13	56.9	1	196-262
1679	TPR	TPR Domain	0.27	17.7	1	28-61
1680	zf-C2H2	Zinc finger, C2H2 type	1.2e-88	307.9	11	140-162:168-190:196-218:224-246:252-274:280-302:308-330:336-358:364-386:392-413:419-441
1680	zf-BED	BED zinc finger	0.96	1.7	3	209-247:321-359:404-442
1680	FYVE	FYVE zinc finger	3.1	-21.2	1	246-319
1680	PHD	PHD-finger	4.4	-15.8	1	253-316
1680	LIM	LIM domain	5.7	-18.1	1	142-206
1680	DAG_PE-bind	Phorbol esters/diacylglycerol binding dom	9.2	-15.5	1	270-325
1681	FYVE	FYVE zinc finger	2.9	-20.9	1	38-98
1683	filament	Intermediate filament protein	1.2e-31	118.6	1	8-270
1683	KE2	KE2 family protein	6.3	-46.3	1	28-136
1684	homeobox	Homeobox domain	1.7e-26	101.5	1	87-143
1685	SPRY	SPRY domain	4e-23	90.2	1	95-231
1688	HTH_3	Helix-turn-helix	2.9e-09	44.2	1	26-79
1688	Peptidase_S24	Peptidase family S24	7.9	-35.2	1	118-237
1689	SET	SET domain	4.9e-52	186.3	1	819-948
1690	lipocalin	Lipocalin / cytosolic fatty-acid binding pr	3.2e-11	50.7	1	1-135
1691	Atrophin-1	Atrophin-1 family	6.2	-673.1	1	147-928
1692	zf-C2H2	Zinc finger, C2H2 type	1.5e-74	261.1	9	109-131:137-159:165-187:193-215:221-243:249-271:277-299:305-327:333-355
1692	zf-BED	BED zinc finger	0.57	3.7	1	122-160

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1692	FYVE	FYVE zinc finger	2.9	-21.0	1	243-319
1692	TFIIS	Transcription factor S-II (TFIIS)	7.7	-6.2	1	137-175
1692	zf-TRAF	TRAF-type zinc finger	8.8	-9.3	1	187-238
1693	dCMP_cyt_deam	Cytidine and deoxycytidylate deaminase	2.2	-23.0	1	1-87
1695	spectrin	Spectrin repeat	2.3	-13.5	1	90-188
1695	K-box	K-box region	5.4	-39.8	1	100-192
1696	Ribosomal_L18e	Eukaryotic ribosomal protein L18	3.3e-08	3.4	1	3-114
1699	kinesin	Kinesin motor domain	1.8e-16	41.0	1	52-225
1700	zf-C2H2	Zinc finger, C2H2 type	4.3e-16	66.9	4	49-71:77-104:110-132:138-161
1703	GoLoco	LGN motif, putative GEF specific for G-alpha	5.8	3.8	1	37-59
1707	DDHD	DDHD domain	4.1e-67	236.4	1	390-594
1709	zf-C2H2	Zinc finger, C2H2 type	6.8e-63	222.4	10	138-160:166-188:194-216:222-244:250-272:278-300:306-328:334-356:362-384:390-413
1709	TFIIS	Transcription factor S-II (TFIIS)	0.47	4.1	1	166-204
1709	zf-BED	BED zinc finger	6.1	-5.4	1	372-414
1709	E6	Early Protein (E6)	9.6	-69.4	1	196-283
1710	zf-C2H2	Zinc finger, C2H2 type	1.2e-70	248.1	11	138-160:166-188:194-216:222-244:250-272:278-300:306-328:334-356:362-384:390-412:418-441
1710	TFIIS	Transcription factor S-II (TFIIS)	0.46	4.2	1	166-204
1710	zf-BED	BED zinc finger	4.3	-4.1	1	172-217
1710	PHD	PHD-finger	9.1	-18.7	1	195-255
1710	E6	Early Protein (E6)	9.6	-69.4	1	224-311
1711	ERM	Ezrin/radixin/moesin family	8.5e-219	740.3	1	208-611
1711	Band_41	FERM domain (Band 4.1 family)	1.8e-135	463.4	1	7-206
1711	MMTV_SA_g	Mouse mammary tumor virus superantigen	1.4	-108.6	1	60-349
1712	ERM	Ezrin/radixin/moesin family	8.5e-219	740.3	1	176-579
1712	Band_41	FERM domain (Band 4.1 family)	2.9e-98	339.9	1	7-174
1712	MMTV_SA_g	Mouse mammary tumor virus superantigen	1.2	-107.6	1	21-317
1713	ERM	Ezrin/radixin/moesin family	8.5e-219	740.3	1	225-628
1713	Band_41	FERM domain (Band 4.1 family)	2.5e-126	433.1	1	7-223

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		family)				
1713	MMTV_SA g	Mouse mammary tumor virus superantigen	1.4	-108.6	1	77-366
1714	Peptidase_C 48	Ulp1 protease family, C- terminal cataly	7.5e-22	86.0	1	1-224
1715	zf-C2H2	Zinc finger, C2H2 type	2e-92	320.4	11	193-215:221- 243:249- 271:277- 299:305- 327:333- 355:361- 383:389- 411:417- 439:445- 467:473-495
1715	KRAB	KRAB box	0.1	9.5	1	38-78
1715	LIM	LIM domain	3.7	-16.5	1	363-427
1717	BTB	BTB/POZ domain	2.3e-33	124.3	1	14-122
1717	zf-C2H2	Zinc finger, C2H2 type	2.7e-08	41.0	2	282-304:310- 333
1717	K_tetra	K ⁺ channel tetramerisation domain	0.25	-27.7	1	32-119
1717	zf-BED	BED zinc finger	7.5	-6.3	1	295-334
1717	Ribosomal_ L44	Ribosomal protein L44	7.8	-22.8	1	211-307
1718	Gag_MA	Matrix protein (MA), p15	0.021	-32.4	1	2-154
1723	GCR	Glucocorticoid receptor	2.2e-302	1017.9	1	26-394
1725	Exo_endo_p hos	Endonuclease/Exonuclease/ph osphatase fa	2.9e-45	163.8	1	52-298
1728	HLH	Helix-loop-helix DNA- binding domain	0.0082	21.4	1	48-100
1728	CTF_NFI	CTF/NF-I family	5.6	-327.4	1	1-451
1729	SCAN	SCAN domain	5.6e-46	166.2	1	39-131
1731	arginase	Arginase family	4.3e-56	199.8	1	69-347
1732	GLFV_dehy drog_N	Glu/Leu/Phe/Val dehydrogenase, dimeri	8.1e-70	245.4	1	44-176
1732	GLFV_dehy drog	Glutamate/Leucine/Phenylalan ine/Valin	3.8	-115.0	1	195-284
1733	cyclin	Cyclin, N-terminal domain	0.94	-18.8	1	54-178
1734	FCH	Fes/CIP4 homology domain	1.6e-26	101.6	1	18-113
1734	SH3	SH3 domain	6.6e-13	56.3	1	572-628
1734	HR1	Hr1 repeat	0.91	6.6	1	435-510
1734	spectrin	Spectrin repeat	2.8	-14.6	1	398-500
1737	wnt	wnt family	1.6e-90	314.2	1	1-297
1738	wnt	wnt family	9.4e-100	344.8	1	92-401
1740	Armadillo_s eg	Armadillo/beta-catenin-like repeat	2.6	13.4	4	480-526:528- 570:640- 679:682-724
1742	PWWP	PWWP domain	0.32	-3.5	1	143-215
1742	PFEMP	Plasmodium falciparum erythrocyte membrane p	4.9	-83.7	1	335-408
1743	G-patch	G-patch domain	2e-12	54.7	1	235-279
1744	Kelch	Kelch motif	4.9e-49	176.3	5	366-408:410- 455:457- 503:505- 545:547-593
1744	BTB	BTB/POZ domain	2.5e-30	114.2	1	62-169

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1746	LRR	Leucine Rich Repeat	5.9e-29	109.6	9	22-45:46-69:70-93:94-117:118-140:141-162:345-368:369-392:393-416
1746	LRRCT	Leucine rich repeat C-terminal domain	3.8e-08	40.5	1	175-225
1746	LRRNT	Leucine rich repeat N-terminal domain	3	9.4	1	285-317
1747	SART-1	SART-1 family	4.7	-353.4	1	23-666
1747	Exonuc_VII_S	Exonuclease VII small subunit	10	-25.5	1	231-294
1752	Circo_ORF_2	Circovirus ORF-2 protein	5.2	-70.8	1	486-705
1752	Sigma54_factors	Sigma-54 factors family	9.6	-351.6	1	556-885
1758	2OG-FeII_Oxy	2OG-Fe(II) oxygenase superfamily	2.2e-12	54.6	1	278-376
1759	Ski_Sno	SKI/SNO/DAC family	6.7e-56	199.1	1	27-155
1761	Nucleoplasmin	Nucleoplasmin	3.8	-93.0	1	316-424
1762	ELM2	ELM2 domain	1.6e-09	45.1	1	174-233
1762	myb_DNA-binding	Myb-like DNA-binding domain	5.4e-06	33.3	1	279-325
1767	TPR	TPR Domain	0.56	16.7	2	89-122:123-156
1769	WH1	WH1 domain	0.0017	11.6	1	11-119
1770	OLF	Olfactomedin-like domain	1.3e-40	148.4	1	182-426
1770	Collagen	Collagen triple helix repeat (20 copies)	1.7e-07	38.4	2	23-81:82-142
1772	Kelch	Kelch motif	2.9e-48	173.8	6	166-212:214-263:265-311:313-359:361-401:403-453
1775	LRR	Leucine Rich Repeat	9.6e-22	85.7	7	26-48:49-71:72-94:95-117:118-140:141-163:164-185
1776	spectrin	Spectrin repeat	0.54	-6.3	1	37-129
1777	dUTPase	dUTPase	2.7e-36	134.0	1	115-235
1777	rvp	Retroviral aspartyl protease	5.4e-25	96.5	1	247-348
1778	homeobox	Homeobox domain	4.1e-30	113.5	1	186-242
1779	K-box	K-box region	4.4	-38.7	1	151-223
1786	filament	Intermediate filament protein	1.3	-188.1	1	203-439
1786	UPF0147	Uncharacterised protein family (UPF0147)	8.4	-38.2	1	177-255
1786	spectrin	Spectrin repeat	8.8	-20.2	1	245-350
1788	homeobox	Homeobox domain	0.023	3.2	1	72-130
1790	LRR	Leucine Rich Repeat	9.3e-10	45.8	5	66-87:88-109:110-131:132-153:157-177
1792	rrm	RNA recognition motif.	8.7e-102	351.6	4	70-141:158-

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						227:250-320:353-422
1793	FYVE	FYVE zinc finger	8.2e-19	75.9	1	46-110
1794	Paralemmin	Paralemmin	2.8e-07	-1.6	1	18-242
1798	DUF298	Domain of unknown function (DUF298)	7.1e-37	135.9	1	159-278
1800	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.23	5.8	1	655-699
1801	zf-C2H2	Zinc finger, C2H2 type	4.8e-60	212.9	7	209-231:237-259:265-287:293-315:321-343:349-371:377-399
1801	KRAB	KRAB box	1.7e-16	68.2	1	1-34
1801	zf-BED	BED zinc finger	1	1.5	1	222-260
1801	FYVE	FYVE zinc finger	5.2	-23.4	1	313-388
1801	TFIIS	Transcription factor S-II (TFIIS)	8.5	-6.5	1	293-331
1801	LIM	LIM domain	8.6	-19.6	1	295-359
1804	2OG-FeII_Oxy	2OG-Fe(II) oxygenase superfamily	4.1e-08	40.4	1	96-227
1807	SH3	SH3 domain	2.1e-15	64.6	1	169-225
1807	LIM	LIM domain	2.7e-11	50.9	1	5-62
1807	Nebulin	Nebulin repeat	2.9e-07	37.6	1	67-95
1808	pkinase	Protein kinase domain	8e-77	268.6	1	73-357
1811	Rhodanese	Rhodanese-like domain	2.4e-65	230.5	2	36-158:185-302
1815	zf-C2H2	Zinc finger, C2H2 type	2.6e-16	67.6	3	96-118:124-146:152-174
1815	PHD	PHD-finger	7.3	-17.9	1	97-132
1818	zf-C2H2	Zinc finger, C2H2 type	1.3e-111	384.2	16	22-44:84-106:112-134:140-162:168-190:196-218:224-246:252-274:280-302:308-330:336-358:364-386:392-414:516-538:544-566:572-594
1818	DM-domain	DM DNA binding domain	3	-8.6	1	194-242
1818	TFIIS	Transcription factor S-II (TFIIS)	3.3	-3.1	1	280-318
1818	zf-UBR1	Putative zinc finger in N-recognin	4.3	-21.1	1	187-245
1818	zf-TRAF	TRAF-type zinc finger	5	-6.6	1	186-239
1818	LIM	LIM domain	7	-18.8	1	198-250
1818	PHD	PHD-finger	8.7	-18.5	1	253-316
1818	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	8.8	-7.9	1	86-117
1821	DnaJ	DnaJ domain	3.6e-24	93.7	1	15-82

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Table 4B

1822	Terpene_sy nth	Terpene synthase family	8.3	-113.9	1	65-270
1823	UQ_con	Ubiquitin-conjugating enzyme	3.8e-39	143.5	1	2-117
1824	zf-C2H2	Zinc finger, C2H2 type	5.7e-112	385.4	19	224-246:252- 274:297- 319:326- 348:360- 382:469- 491:497- 519:525- 547:588- 610:616- 638:711- 733:739- 761:767- 789:795- 817:823- 845:851- 873:879- 901:908- 930:936-958
1824	TFIIS	Transcription factor S-II (TFIIS)	1.8	-0.9	1	297-336
1824	PHD	PHD-finger	2.6	-13.7	1	253-305
1824	LIM	LIM domain	3.6	-16.4	1	910-962
1824	zf-BED	BED zinc finger	4.3	-4.1	1	864-902
1824	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	6.6	-6.8	1	910-941
1824	Ribosomal_ L34e	Ribosomal protein L34e	7.6	-37.7	1	708-789
1825	dNK	Deoxynucleoside kinase	7.6	-47.8	1	221-346
1830	zf-C2H2	Zinc finger, C2H2 type	1.4e-59	211.4	8	82-104:120- 142:148- 170:176- 198:204- 226:232- 254:260- 282:288-310
1830	zf-BED	BED zinc finger	3.1	-2.9	1	132-171
1830	TFIIS	Transcription factor S-II (TFIIS)	5.3	-4.8	1	232-270
1830	PHD	PHD-finger	5.7	-16.9	1	83-156
1830	FYVE	FYVE zinc finger	6	-24.1	1	76-159
1831	ketoacyl- synt_C	Beta-ketoacyl synthase, C- terminal do	0.21	-71.5	1	145-294
1834	SCAN	SCAN domain	1.6e-64	227.7	1	46-141
1834	zf-C2H2	Zinc finger, C2H2 type	3e-12	54.1	2	251-273:279- 301
1834	rvt	Reverse transcriptase	4.5	-55.7	1	372-496
1834	FYVE	FYVE zinc finger	9	-25.8	1	245-290
1836	MAGE	MAGE family	9.8	-139.8	1	133-354
1838	DM-domain	DM DNA binding domain	3.8e-25	97.0	1	93-139
1838	DMA	DMRTA motif	1.8e-23	91.4	1	326-364
1838	zf-MYND	MYND finger	5.4	-10.4	1	86-116
1839	FYVE	FYVE zinc finger	5.1	-23.4	1	49-114
1840	FYVE	FYVE zinc finger	5.1	-23.4	1	49-114
1841	FYVE	FYVE zinc finger	5.1	-23.4	1	49-114

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Table 4B

1842	FYVE	FYVE zinc finger	5.1	-23.4	1	49-114
1846	UBX	UBX domain	7.8e-10	46.1	1	168-247
1849	LIM	LIM domain	0.00011	21.6	1	72-117
1850	Rota_NS26	Rotavirus NS26	4	-106.8	1	112-327
1850	CUE	CUE domain	7.3	5.1	1	31-73
1850	Tropomyosi n	Tropomyosin	7.7	-119.0	1	216-395
1850	AUX_IAA	AUX/IAA family	8.3	-131.0	1	330-490
1852	zf-B_box	B-box zinc finger	6.1e-08	39.8	1	122-164
1852	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.00052	26.8	1	26-84
1852	PHD	PHD-finger	0.65	-8.2	1	25-87
1852	spectrin	Spectrin repeat	8	-19.7	1	209-300
1852	SMC_C	SMC family, C-terminal domain	8.5	-134.5	1	189-317
1854	mito_carr	Mitochondrial carrier protein	2.5e-64	227.1	3	20-143:146- 243:246-341
1856	zf-C2H2	Zinc finger, C2H2 type	3.3e-50	180.2	9	464-487:491- 514:518- 541:548- 570:576- 598:604- 626:632- 654:660- 682:688-710
1856	BTB	BTB/POZ domain	4.5e-24	93.4	1	32-141
1856	zf-BED	BED zinc finger	0.7	2.9	1	641-683
1856	FYVE	FYVE zinc finger	7.6	-25.1	1	540-615
1856	DAG_PE- bind	Phorbol esters/diacylglycerol binding d	8.1	-15.0	1	541-581
1856	Ribosomal_ L31	Ribosomal protein L31	9.9	-25.1	1	567-620
1857	Smg4_UPF 3	Smg-4/UPF3 family	1.3e-101	351.0	1	60-228
1857	rrm	RNA recognition motif.	5.1	-5.0	1	70-143
1857	KNOX2	KNOX2 domain	6.5	-8.7	1	167-211
1859	TGT	Queuine tRNA- ribosyltransferase	9.7e-19	75.7	1	127-412
1860	Myosin_tail	Myosin tail	0.00052	-136.5	1	1-498
1860	filament	Intermediate filament protein	0.9	-183.5	1	112-412
1860	Tropomyosi n	Tropomyosin	8	-119.2	1	247-505
1861	LRR	Leucine Rich Repeat	9.3e-10	45.8	5	66-87:88- 109:110- 131:132- 153:157-177
1862	efhand	EF hand	0.12	18.9	1	483-511
1863	trypsin	Trypsin	5.1e-79	275.9	1	21-246
1869	FH2	Formin Homology 2 Domain	1.6e-54	194.5	1	87-527
1869	GST_C	Glutathione S-transferase, C- terminal d	2.7	-4.9	1	153-286
1869	Peptidase_C 48	Ulp1 protease family, C- terminal cataly	7.5	-42.6	1	354-1047
1869	TP2	Nuclear transition protein 2	9.7	-60.8	1	516-610
1871	LRR	Leucine Rich Repeat	4.4	13.7	3	473-496:501- 523:557-581
1873	Josephin	Josephin	8.7e-10	46.0	1	13-145

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Table 4B

1874	GTP_EFTU	Elongation factor Tu GTP binding domain	1.2e-18	75.4	1	5-217
1874	GTP_EFTU_D2	Elongation factor Tu domain 2	8.7e-11	49.3	1	229-305
1875	GTP_EFTU	Elongation factor Tu GTP binding domain	1.3e-71	251.3	1	17-367
1875	EFG_C	Elongation factor G C-terminus	3.9e-23	90.3	1	979-1067
1875	GTP_EFTU_D2	Elongation factor Tu domain 2	6	-0.1	1	497-599
1876	helicase_C	Helicase conserved C-terminal domain	5e-19	76.6	1	748-826
1876	DEAD	DEAD/DEAH box helicase	5.8e-13	56.5	1	298-531
1876	CARD	Caspase recruitment domain	0.36	9.2	1	111-200
1876	SART-1	SART-1 family	6.1	-357.6	1	240-906
1880	KRAB	KRAB box	8.3e-27	102.5	1	7-47
1881	Dishevelled	Dishevelled specific domain	0.85	1.5	1	873-945
1881	GrpE	GrpE	6.3	-84.4	1	430-661
1883	LIM	LIM domain	4.2e-50	179.9	2	5-61:64-124
1883	homeobox	Homeobox domain	1.9e-25	98.0	1	181-237
1885	zf-C2H2	Zinc finger, C2H2 type	9.9e-30	112.2	6	157-180:231-253:259-281:386-408:414-436:445-468
1885	zf-C4	Zinc finger, C4 type (two domains)	3.2	-51.4	1	386-446
1885	zf-BED	BED zinc finger	8.6	-6.8	1	427-469
1886	PH	PH domain	0.00021	28.0	1	21-128
1888	homeobox	Homeobox domain	4.4e-09	43.6	1	207-258
1888	PTS_EIIA_2	Phosphoenolpyruvate-dependent sugar pho	7.9	-70.4	1	30-136
1888	Cathelicidins	Cathelicidin	7.9	-1.7	1	119-184
1889	FHA	FHA domain	8.6	-5.9	1	127-273
1890	zf-C2H2	Zinc finger, C2H2 type	1.5e-118	407.2	18	194-216:222-244:250-272:278-300:306-328:362-384:390-412:418-440:446-468:474-498:508-530:536-558:564-586:592-614:620-642:648-670:676-698:704-726
1890	KRAB	KRAB box	1.4e-23	91.7	1	24-64
1890	zf-BED	BED zinc finger	0.87	2.1	1	291-329
1890	TFIIS	Transcription factor S-II (TFIIS)	2.5	-2.1	1	676-714
1890	LIM	LIM domain	3.5	-16.3	1	196-255

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Table 4B

1890	GATA	GATA zinc finger	6.2	-10.6	1	416-462
1891	KRAB	KRAB box	3.9e-08	40.5	1	22-50
1892	MyTH4	MyTH4 domain	7.3e-24	92.7	1	74-180
1892	Band_41	FERM domain (Band 4.1 family)	7.1	-113.6	1	202-384
1895	IF4E	Eukaryotic initiation factor 4E	1.5e-99	344.1	1	19-242
1896	ank	Ankyrin repeat	5.4	13.1	1	9-39
1898	zf-C2H2	Zinc finger, C2H2 type	1.5e-63	224.6	8	268-290:296-318:324-346:352-374:380-402:408-430:436-458:464-486
1898	SCAN	SCAN domain	3.5e-52	186.8	1	43-138
1898	zf-BED	BED zinc finger	2	-1.1	1	449-487
1898	TFIIS	Transcription factor S-II (TFIIS)	5.5	-4.9	1	352-390
1898	E6	Early Protein (E6)	7.1	-67.8	1	298-385
1899	zf-C4	Zinc finger, C4 type (two domains)	2.5e-08	12.5	1	278-326
1900	Mra1	Suppressor Mra1	3.7e-79	276.4	1	77-239
1901	Mra1	Suppressor Mra1	1e-40	148.7	1	77-189
1903	HEAT	HEAT repeat	5.4e-13	56.6	3	6-45:46-84:85-123
1907	DUF75	Protein of unknown function DUF75	8.3	-98.9	1	4-152
1908	TPR	TPR Domain	0.88	15.9	4	57-90:91-124:151-184:230-263
1911	KH-domain	KH domain	0.11	13.4	1	63-115
1913	homeobox	Homeobox domain	0.0062	9.0	1	289-348
1913	KNOX2	KNOX2 domain	1.7	-3.9	1	120-171
1915	RNA_capsid	Calicivirus putative RNA polymerase/capsid	1.9	-101.3	1	618-819
1916	RNA_capsid	Calicivirus putative RNA polymerase/capsid	3.2	-105.0	1	618-801
1917	kinesin	Kinesin motor domain	7.7e-67	235.5	1	1-228
1918	zf-C4	Zinc finger, C4 type (two domains)	1.7e-08	13.8	1	151-192
1921	rnaseH	RNase H	9.3e-14	59.1	1	31-167
1924	Ribosomal_S8	Ribosomal protein S8	4.6e-34	126.6	1	5-130
1926	zf-C2H2	Zinc finger, C2H2 type	1.3e-69	244.7	8	184-206:212-234:240-262:268-290:296-318:324-346:352-374:380-402
1926	KRAB	KRAB box	1.3e-24	95.2	1	8-48
1926	zf-BED	BED zinc finger	1.4	0.2	1	197-235
1926	LIM	LIM domain	3.7	-16.5	1	326-390
1926	TFIIS	Transcription factor S-II (TFIIS)	4.1	-3.9	1	240-278
1926	zf-MIZ	MIZ zinc finger	9.9	-21.4	1	197-251
1927	filament	Intermediate filament protein	4.7e-120	412.3	1	110-423

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Table 4B

1927	AnfG_VnfG	Vanadium/alternative nitrogenase delta	7.4	-61.9	1	232-316
1927	Transposase 8	Transposase	8.5	-18.0	1	273-361
1928	zf-C2H2	Zinc finger, C2H2 type	2.4e-67	237.1	10	199-227:282-304:310-332:338-360:366-388:394-416:422-444:450-472:478-500:506-528
1928	KRAB	KRAB box	6e-23	89.7	1	39-79
1928	zf-BED	BED zinc finger	3.8	-3.6	2	323-361:491-529
1929	zf-C2H2	Zinc finger, C2H2 type	7.4e-155	527.9	18	178-200:206-228:234-256:262-284:290-312:318-340:346-368:374-396:402-424:430-452:458-480:486-508:514-536:542-564:570-592:598-620:626-648:654-676
1929	KRAB	KRAB box	9.6e-28	105.6	1	8-48
1929	Avirulence	Xanthomonas avirulence protein, Avr/PthA	1.7	-167.6	1	235-616
1929	TFIIS	Transcription factor S-II (TFIIS)	3.2	-3.0	1	318-356
1929	zf-MIZ	MIZ zinc finger	6.3	-19.8	1	523-581
1929	zf-BED	BED zinc finger	9.4	-7.1	2	359-397:611-649
1930	zf-C2H2	Zinc finger, C2H2 type	1.5e-95	330.8	14	348-370:376-398:404-426:432-454:488-510:516-538:544-566:572-594:600-622:628-650:656-678:712-734:740-762:768-790
1930	KRAB	KRAB box	2.4e-50	180.7	2	13-53:110-150
1930	LIM	LIM domain	0.57	-9.7	1	546-600

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Table 4B

1930	DM-domain	DM DNA binding domain	7.6	-12.2	1	598-648
1930	zf-BED	BED zinc finger	9.4	-7.1	2	501-539:585-623
1932	zf-C2H2	Zinc finger, C2H2 type	2.2e-36	134.3	6	63-85:91-113:119-141:147-169:177-199:213-235
1932	zf-TRAF	TRAF-type zinc finger	7.1	-8.3	1	113-163
1933	zf-C2H2	Zinc finger, C2H2 type	3.3e-117	402.8	14	368-390:396-418:424-446:452-474:480-502:508-530:536-558:564-586:592-614:620-642:648-670:676-698:704-726:732-754
1933	SCAN	SCAN domain	3.3e-53	190.2	1	43-138
1933	KRAB	KRAB box	1.4e-17	71.8	1	170-210
1933	zf-BED	BED zinc finger	0.55	3.8	1	577-615
1933	TFIIS	Transcription factor S-II (TFIIS)	2.7	-2.3	1	368-406
1933	Ribosomal_L34e	Ribosomal protein L34e	7.4	-37.6	1	362-446
1936	HLH	Helix-loop-helix DNA-binding domain	2.6e-21	84.2	1	67-118
1937	zf-C2H2	Zinc finger, C2H2 type	1.1e-159	543.8	21	190-212:218-240:246-268:274-296:302-324:330-352:358-380:386-408:414-436:442-464:470-492:498-520:526-548:554-576:582-604:610-632:638-660:666-688:694-716:722-744:750-772
1937	FYVE	FYVE zinc finger	2.5	-20.3	1	377-453
1937	HNH	HNH endonuclease	3.5	3.7	1	330-383
1937	TFIIS	Transcription factor S-II (TFIIS)	4	-3.8	1	638-676
1937	zf-BED	BED zinc finger	6.7	-5.8	1	371-409
1937	LIM	LIM domain	8.5	-19.5	1	332-384

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Table 4B

1938	CUB	CUB domain	1.4e-38	141.6	2	127-256:325-419
1938	sushi	Sushi domain (SCR repeat)	5.3e-16	66.6	2	61-117:264-321
1939	sushi	Sushi domain (SCR repeat)	1.3e-09	45.4	1	113-170
1940	MotA_ExbB	MotA/TolQ/ExbB proton channel family	1.6	-49.6	1	52-174
1941	IBR	IBR domain	1.8e-17	71.5	2	1969-2032:2054-2108
1941	APC10	Anaphase-promoting complex, subunit 10	0.045	-70.7	1	968-1150
1941	ICln_channel	Nucleotide-sensitive chloride conductance	1.6	-12.1	1	1435-1513
1941	Cullin	Cullin family	1.9	-383.6	1	993-1782
1941	LIM	LIM domain	5	-17.6	1	2065-2110
1942	Ribosomal_S4	Ribosomal protein S4/S9 N-terminal domain	1.2e-26	101.9	1	1-89
1942	S4	S4 domain	1.1e-10	48.9	1	90-137

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
972	1bab	A	1	122	2.4e-48			173.65	OXYGEN TRANSPORT HEMOGLOBIN THIONVILLE ALPHA CHAIN MUTANT WITH VAL 1 IBAB 3 REPLACED BY GLU AND AN ACETYLATED MET BOUND TO THE IBAB 4 AMINO TERMINUS IBAB 5	
972	1bab	A	1	122	2.4e-48	0.66	1.00		OXYGEN TRANSPORT HEMOGLOBIN THIONVILLE ALPHA CHAIN MUTANT WITH VAL 1 IBAB 3 REPLACED BY GLU AND AN ACETYLATED MET BOUND TO THE IBAB 4 AMINO TERMINUS IBAB 5	
972	1gcw	A	3	122	1.2e-48	0.71	1.00		HEMOGLOBIN; CHAIN: A, C; HEMOGLOBIN; CHAIN: B, D;	OXYGEN STORAGE/TRANSPORT HEMOGLOBIN, CARBON MONOXIDE BOUND FORM
972	1hda	A	2	122	2.4e-47			157.67	OXYGEN TRANSPORT HEMOGLOBIN (DEOXY) 1HDA 3	
972	1hda	A	2	122	2.4e-47	0.68	1.00		OXYGEN TRANSPORT HEMOGLOBIN (DEOXY) 1HDA 3	
973	2cev	A	6	287	1.2e-79	0.90	1.00		ARGINASE; CHAIN: A, B, C, D, E, F;	HYDROLASE ENZYME, HYDROLASE, ARGININE HYDROLYSIS, NITROGEN METABOLISM, 2 MANGANESE METALLOENZYME
973	2cev	A	6	289	1.2e-79			205.84	ARGINASE; CHAIN: A, B, C, D, E, F;	HYDROLASE ENZYME, HYDROLASE, ARGININE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										HYDROLYSIS, NITROGEN METABOLISM, 2 MANGANESE METALLOENZYME
974	1d3v	A	6	295	0			431.79	ARGINASE; CHAIN: A, B;	HYDROLASE BINUCLEAR MANGANESE CLUSTER, BORONIC ACID INHIBITOR, 2 PERFECTLY TWINNED CRYSTAL, HYDROLASE
974	1d3v	A	6	295	0	1.07	1.00		ARGINASE; CHAIN: A, B;	HYDROLASE BINUCLEAR MANGANESE CLUSTER, BORONIC ACID INHIBITOR, 2 PERFECTLY TWINNED CRYSTAL, HYDROLASE
975	2cev	A	6	286	4.8e-86	1.10	1.00		ARGINASE; CHAIN: A, B, C, D, E, F;	HYDROLASE ENZYME, HYDROLASE, ARGININE HYDROLYSIS, NITROGEN METABOLISM, 2 MANGANESE METALLOENZYME
975	2cev	A	6	290	4.8e-86			223.29	ARGINASE; CHAIN: A, B, C, D, E, F;	HYDROLASE ENZYME, HYDROLASE, ARGININE HYDROLYSIS, NITROGEN METABOLISM, 2 MANGANESE METALLOENZYME
979	1aqc	A	593	713	1.2e-07	0.18	0.94		X11; CHAIN: A, B; PEPTIDE; CHAIN: C, D	COMPLEX (PEPTIDE BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										MODULE/PEPTIDE), PEPTIDE BINDING 2 MODULE, PTB DOMAIN
979	1aqc	B	473	544	0.006	-0.60	0.03		X11; CHAIN: A, B; PEPTIDE; CHAIN: C, D	COMPLEX (PEPTIDE BINDING MODULE/PEPTIDE), PEPTIDE BINDING 2 MODULE, PTB DOMAIN
979	1ddm	A	419	534	3.6e-07	0.04	0.16		NUMB PROTEIN; CHAIN: A; NUMB ASSOCIATE KINASE; CHAIN: B;	SIGNALING PROTEIN/TRANSFERASE NAK; COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMMETRIC CELL DIVISION
979	1ddm	A	593	711	8.4e-25	0.29	1.00		NUMB PROTEIN; CHAIN: A; NUMB ASSOCIATE KINASE; CHAIN: B;	SIGNALING PROTEIN/TRANSFERASE NAK; COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMMETRIC CELL DIVISION
979	1e0m	A	292	321	0.00012	0.20	0.59		WWPROTOTYPE; CHAIN: A;	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN
979	1f8a	B	290	323	0.00012	0.45	0.71		PEPTIDYL-PROLYL CIS-TRANS ISOMERASE NIMA- CHAIN: B; Y(SEP)PT(SEP)S PEPTIDE; CHAIN: C;	ISOMERASE PIN1; PEPTIDYL-PROLINE ISOMERASE, WW DOMAIN, PHOSPHOSERINE BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
979	1pin	A	293	321	0.0012	0.14	0.76		PEPTIDYL-PROLYL CIS-TRANS ISOMERASE; CHAIN: A; ALA-PRO DIPEPTIDE; CHAIN: B;	COMPLEX (ISOMERASE/DIPEPTIDE) PIN1; PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, ROTAMASE, 2 COMPLEX (ISOMERASE/DIPEPTIDE) CONNECT
979	1x11	A	593	713	1.2e-08	-0.01	0.66		X11; CHAIN: A, B; 13-MER PEPTIDE; CHAIN: C, D;	COMPLEX (PEPTIDE BINDING MODULE/PEPTIDE), PTB DOMAIN
980	1aqc	A	572	692	1.2e-07	0.18	0.94		X11; CHAIN: A, B; PEPTIDE; CHAIN: C, D	COMPLEX (PEPTIDE BINDING MODULE/PEPTIDE), PEPTIDE BINDING 2 MODULE, PTB DOMAIN
980	1ddm	A	398	513	3.6e-07	0.04	0.16		NUMB PROTEIN; CHAIN: A; NUMB ASSOCIATE KINASE; CHAIN: B;	SIGNALING PROTEIN/TRANSFERASE NAK; COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMMETRIC CELL DIVISION
980	1ddm	A	572	690	8.4e-25	0.29	1.00		NUMB PROTEIN; CHAIN: A; NUMB ASSOCIATE KINASE; CHAIN: B;	SIGNALING PROTEIN/TRANSFERASE NAK; COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB),

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										ASYMMETRIC CELL DIVISION
980	1e0m	A	292	321	0.00012	0.20	0.59		WWPROTOTYPE; CHAIN: A;	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN
980	1f8a	B	290	323	0.00012	0.45	0.71		PEPTIDYL-PROLYL CIS-TRANS ISOMERASE NIMA- CHAIN: B; Y(SEP)PT(SEP)S PEPTIDE; CHAIN: C;	ISOMERASE PIN1; PEPTIDYL-PROLINE ISOMERASE, WW DOMAIN, PHOSPHOSERINE BINDING
980	1pin	A	293	321	0.00012	0.14	0.76		PEPTIDYL-PROLYL CIS-TRANS ISOMERASE; CHAIN: A; ALA-PRO DIPEPTIDE; CHAIN: B;	COMPLEX (ISOMERASE/DIPEPTIDE) PIN1; PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, ROTAMASE, 2 COMPLEX (ISOMERASE/DIPEPTIDE) CONNECT
980	1x11	A	572	692	1.2e-08	-0.01	0.66		X11; CHAIN: A, B; 13-MER PEPTIDE; CHAIN: C, D;	COMPLEX (PEPTIDE BINDING MODULE/PEPTIDE), PTB DOMAIN
986	1a5e		138	240	2.4e-19	0.37	1.00		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
986	1a5e		45	168	1.2e-15	0.23	0.12		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
986	1awc	B	5	138	1.2e-26	0.38	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
986	1awc	B	51	205	2.4e-35			79.92	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
986	1awc	B	53	204	2.4e-30	0.29	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
986	1awc	B	86	237	2.4e-35	0.37	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
986	1bd8		3	106	1.2e-19	0.06	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TRANSCRIPTION 3 FACTOR TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
986	1bd8		52	205	8.4e-28	0.08	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
986	1bd8		52	207	3.6e-33			70.26	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
986	1bd8		86	238	3.6e-33	0.17	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
986	1bi7	B	138	240	2.4e-20	0.14	0.96		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
986	1bi7	B	17	140	1.2e-15	0.35	0.64		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
986	1bi7	B	4	107	8.4e-18	0.14	0.69		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
986	1d9s	A	111	240	2.4e-26	0.19	0.98		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
986	1d9s	A	82	210	8.4e-27	-0.05	0.90		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
986	1d9s	A	9	144	2.4e-23	0.24	0.21		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
986	1ihb	A	16	140	9.6e-23	0.21	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
986	1ihb	A	3	106	1.2e-19	0.05	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
986	1ihb	A	54	208	9.6e-30			62.78	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
986	1ihb	A	56	208	3.6e-28	0.15	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
986	1ihb	A	88	240	9.6e-30	0.24	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
986	1myo		123	234	3.6e-25	0.15	0.88		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
986	1myo		153	240	3.6e-21	-0.06	0.99		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK- REPEAT
986	1myo		21	135	2.4e-20	-0.14	0.92		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK- REPEAT
986	1myo		4	103	3.6e-17	-0.08	0.45		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK- REPEAT
986	1myo		52	173	2.4e-24			57.93	MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK- REPEAT
986	1myo		88	202	2.4e-24	-0.20	0.90		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK- REPEAT
986	1nfi	E	15	210	1.2e-40	0.46	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
986	1nfi	E	15	218	1.2e-40			77.05	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
986	1nfi	E	4	150	2.4e-26	0.02	0.88		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	REPEAT HELIX COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
986	1nfi	E	83	240	1.2e-25	-0.11	0.99		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
987	1alh	A	137	237	5.1e-21	0.02	0.03		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
987	1alh	A	166	238	1.5e-22	0.46	0.05		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
987	1alh	A	185	265	5.1e-26	0.47	1.00		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
987	1alh	A	185	266	2.2e-38	0.12	0.98		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	(ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
987	1mey	C	160	237	1.7e-35	0.30	0.60		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
987	1mey	C	184	265	1.7e-43	0.49	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
987	1mey	C	212	293	5.1e-46	0.10	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
987	1mey	C	240	321	1.7e-47	0.54	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
987	1mey	C	268	349	6.8e-48	0.21	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
987	1mey	C	296	377	6.8e-49	0.36	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
987	1mey	C	324	405	5.1e-49	0.28	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
987	1mey	C	352	433	1.7e-50	0.27	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
987	1mey	C	380	461	1.2e-50	0.38	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
987	1mey	C	408	489	1.5e-50	0.40	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
987	1mey	C	436	517	5.1e-50	0.30	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
987	1mey	C	464	545	1.7e-50	-0.10	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
987	1mey	C	492	573	1.7e-50	0.49	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
987	1mey	C	520	601	8.5e-51	0.29	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
987	1mey	C	520	602	8.5e-51			94.56	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
987	1mey	C	548	620	3.4e-43	0.39	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
987	1mey	G	182	209	3.4e-09	0.32	0.28		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
987	1tf3	A	161	237	5.1e-14	0.16	-0.12		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: E, F;	5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
987	1tf6	A	161	302	5.1e-31	0.09	0.88		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
987	1tf6	A	168	321	2.2e-56	0.04	0.92		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
987	1tf6	A	185	377	4.4e-64	0.04	0.86		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
987	1tf6	A	213	365	8.5e-37	-0.06	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
987	1tf6	A	241	433	6.6e-74	-0.19	0.69		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
987	1tf6	A	297	461	6.6e-72	-0.10	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
987	1tf6	A	381	526	6.8e-36	0.10	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	-Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										INITIATION, ZINC FINGER PROTEIN
987	1tf6	A	408	577	2.2e-77			97.82	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
987	1tf6	A	437	601	2.2e-77	0.04	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
987	1tf6	A	493	611	6.8e-32	0.08	0.77		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
987	1ubd	C	166	265	4.4e-36	0.48	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
987	1ubd	C	166	265	8.5e-28	0.16	0.93		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
987	1ubd	C	192	293	1.7e-31	0.35	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
987	1ubd	C	211	321	1.5e-55	0.03	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
987	1ubd	C	266	405	2.2e-52	-0.00	0.89		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
987	1ubd	C	294	434	1.3e-54	-0.02	0.93		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
987	1ubd	C	332	433	5.1e-35	0.01	0.95		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
987	1ubd	C	350	461	8.8e-55	0.15	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
987	1ubd	C	352	462	4.4e-57			79.95	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
987	1ubd	C	360	461	5.1e-35	0.27	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
987	1ubd	C	388	489	8.5e-36	0.23	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
987	1ubd	C	406	517	4.4e-57	0.15	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
987	1ubd	C	462	573	1.1e-58	0.26	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
987	1ubd	C	490	602	8.8e-60	-0.03	0.92		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
987	1ubd	C	500	601	3.4e-34	-0.07	0.90		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A, B;	INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
987	1ubd	C	518	620	2e-44	0.12	1.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
987	1ubd	C	525	618	8.5e-30	-0.17	0.99		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
987	2gli	A	136	292	3.4e-29	-0.04	0.34		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
987	2gli	A	166	323	2.2e-50	0.17	0.98		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
987	2gli	A	212	351	2.2e-67	0.33	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
987	2gli	A	240	435	4.4e-68	0.02	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
987	2gli	A	304	432	3.4e-34	0.38	0.87		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
987	2gli	A	353	490	1.1e-70	0.05	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
987	2gli	A	464	603	2.2e-76			89.17	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
987	2gli	A	464	603	2.2e-76	0.06	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
987	2gli	A	472	600	1.5e-33	0.31	0.93		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
987	2gli	A	500	620	6.8e-30	0.17	0.80		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
990	1bkf		166	275	1.2e-27			69.27	FK506 BINDING PROTEIN; CHAIN: NULL;	ISOMERASE FKBP; ISOMERASE, ROTAMASE
990	1bkf		169	258	1.2e-27	0.27	1.00		FK506 BINDING PROTEIN; CHAIN: NULL;	ISOMERASE FKBP; ISOMERASE, ROTAMASE
990	1c9h	A	169	258	1.2e-27	0.34	1.00		FKBP12.6; CHAIN: A;	IMMUNE SYSTEM CALCINEURIN; FKBP12, RAPAMYCIN, COMPLEX, RYANODINE RECEPTOR
990	1rot		163	275	4.8e-26			61.20	FKBP59-I; CHAIN: NULL;	ROTAMASE (ISOMERASE) FKBP52 OR HSP56; ROTAMASE (ISOMERASE), DOMAIN I (N-TERM) OF A 59 KDA, 2 FK506-BINDING PROTEIN, PEPTIDYL PROLYL CIS-TRANS ISOMERASE
990	1rot		169	258	4.8e-26	0.07	0.95		FKBP59-I; CHAIN: NULL;	ROTAMASE (ISOMERASE) FKBP52 OR HSP56;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										ROTAMASE (ISOMERASE), DOMAIN I (N-TERM) OF A 59 KDA, 2 FK506-BINDING PROTEIN, PEPTIDYL PROLYL CIS-TRANS ISOMERASE
992	1ass		162	321	8.4e-49	0.63	1.00		THERMOSOME; CHAIN: NULL;	CHAPERONIN CHAPERONIN, HSP60, THERMOSOME, TCP1, GROEL, THERMOPLASMA 2 ACIDOPHILUM, ATP-BINDING
992	1ass		162	322	8.4e-49			97.98	THERMOSOME; CHAIN: NULL;	CHAPERONIN CHAPERONIN, HSP60, THERMOSOME, TCP1, GROEL, THERMOPLASMA 2 ACIDOPHILUM, ATP-BINDING
992	1der	A	12	476	3.6e-72	0.13	1.00		GROEL; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N;	CHAPERONIN HSP60 CLASS, ATP, MAGNESIUM, CHAPERONIN
992	1der	A	9	483	3.6e-72			110.48	GROEL; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N;	CHAPERONIN HSP60 CLASS, ATP, MAGNESIUM, CHAPERONIN
994	1crz	A	200	513	0.00024	0.18	0.07		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
994	1crz	A	387	544	6e-05	0.60	0.53		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
998	1av1	A	5	211	0.0012			51.03	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
998	1fxk	A	101	186	0.00034	0.00	0.00		PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	CHAPERONE ARCHAEAL PROTEIN
999	1dii	A	101	575	2.2e-97	0.58	1.00		P-CRESOL METHYLHYDROXYLASE; CHAIN: A, B; P-CRESOL METHYLHYDROXYLASE; CHAIN: C, D;	OXIDOREDUCTASE PCMH; PCMH; FLAVOCHROME, ELECTRON-TRANSFER, FAD, HEME
999	1dii	A	92	574	6.8e-56	0.51	1.00		P-CRESOL METHYLHYDROXYLASE; CHAIN: A, B; P-CRESOL METHYLHYDROXYLASE; CHAIN: C, D;	OXIDOREDUCTASE PCMH; PCMH; FLAVOCHROME, ELECTRON-TRANSFER, FAD, HEME
999	1e8g	A	136	575	1.5e-52	0.35	1.00		VANILLYL-ALCOHOL OXIDASE; CHAIN: A, B;	OXIDOREDUCTASE ARYL-ALCOHOL OXIDASE, 4-ALLYLPHENOL OXIDASE; FLAVOENZYME, SPECIFICITY
999	1f0x	A	100	574	1.7e-40	0.45	1.00		D-LACTATE DEHYDROGENASE;	OXIDOREDUCTASE DLDH;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
999	1f0x	A	99	574	8.8e-50	0.31	1.00		CHAIN: A, B; D-LACTATE DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE OXIDOREDUCTASE DLDH; OXIDOREDUCTASE
999	1qj2	C	139	245	0.0017	0.03	0.42		CARBON MONOXIDE DEHYDROGENASE; CHAIN: A, G; CARBON MONOXIDE DEHYDROGENASE; CHAIN: B, H; CARBON MONOXIDE DEHYDROGENASE; CHAIN: C, I;	OXIDOREDUCTASE MOLYBDENUM HYDROXYLASE
1007	1sig		119	407	0.0022			61.01	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1007	2adr		28	73	3.4e-09	0.07	-0.17		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
1012	1e08	A	1	340	0	0.48	1.00		[FE]-HYDROGENASE (LARGE SUBUNIT); CHAIN: A; [FE]- HYDROGENASE (SMALL SUBUNIT); CHAIN: D; CYTOCHROME C553; CHAIN: E	HYDROGENASE HYDROGENASE, CYTOCHROME C553, ELECTRON TRANSFER COMPLEX
1012	1feh	A	1	396	0			118.20	PERIPLASMIC HYDROGENASE 1; CHAIN: A;	OXIDOREDUCTASE OXIDOREDUCTASE
1012	1feh	A	2	396	0	0.56	1.00		PERIPLASMIC HYDROGENASE 1; CHAIN: A;	OXIDOREDUCTASE OXIDOREDUCTASE
1012	1hfe	L	1	340	0	0.64	1.00		FE-ONLY HYDROGENASE	HYDROGENASE FE-ONLY

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									(SMALLER SUBUNIT); CHAIN: S, T; FE-ONLY HYDROGENASE (LARGER SUBUNIT); CHAIN: L, M;	HYDROGENASE, X-RAY CRYSTALLOGRAPHY, HYDROGENE 2 METABOLISM, PERIPLASM
1012	1hfe	L	1	345	0			158.84	FE-ONLY HYDROGENASE (SMALLER SUBUNIT); CHAIN: S, T; FE-ONLY HYDROGENASE (LARGER SUBUNIT); CHAIN: L, M;	HYDROGENASE FE-ONLY HYDROGENASE, X-RAY CRYSTALLOGRAPHY, HYDROGENE 2 METABOLISM, PERIPLASM
1015	1a17		264	362	5.1e-13	-0.00	0.80		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRA TRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN- PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1015	1a17		295	432	5.1e-12	-0.05	0.17		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRA TRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN- PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1015	1a17		345	481	8.8e-07	0.04	0.33		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRA TRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN- PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1015	1a17		403	539	1e-12	-0.04	0.29		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN- PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1015	1a17		444	571	6.8e-11	0.25	-0.07		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN- PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1015	1a17		603	731	1.7e-09	0.06	-0.03		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN- PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1015	1a17		623	745	5.1e-15	0.34	0.72		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN- PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1015	1a17		664	768	6.8e-15	0.47	0.81		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1015	1d8d	A	624	757	2.2e-09	0.35	0.51		FARNESYLTRANSFERASE (ALPHA SUBUNIT); CHAIN: A; FARNESYLTRANSFERASE (BETA SUBUNIT); CHAIN: B; K-RAS4B PEPTIDE SUBSTRATE; CHAIN: P;	TRANSFERASE FTASE; FTASE; FTASE, PFT, PFTASE, FARNESYLTRANSFERASE, FARNESYL 2 TRANSFERASE, CAAAX, RAS, CANCER
1015	1dce	A	603	728	0.0024	-0.16	0.00		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1015	1e96	B	2	107	1.4e-05	-0.22	0.12		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1015	1e96	B	264	432	1.4e-09	0.11	-0.07		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1015	1e96	B	630	761	1.7e-10	0.25	0.60		RAS-RELATED C3 BOTULINUM	SIGNALLING COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	RAC1; P67PHOX; SIGNALING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1015	1elr	A	263	361	1.7e-13.	-0.08	0.09		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1015	1elr	A	298	391	1.4e-11	0.00	0.12		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1015	1elr	A	602	684	1e-08	0.28	-0.02		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1015	1elr	A	629	721	1.5e-13	0.34	0.96		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1015	1elr	A	663	752	6.8e-13	0.45	0.62		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1015	1elw	A	264	366	1.7e-11	0.19	0.48		TPR1-DOMAIN OF HOP; CHAIN:	CHAPERONE HOP, TPR-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									A, B; HSC70-PEPTIDE; CHAIN: C, D;	DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1015	1elw	A	295	399	5.1e-13	0.43	0.64		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1015	1elw	A	340	444	1.2e-06	0.04	0.05		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1015	1elw	A	410	524	1.7e-12	0.26	0.98		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1015	1elw	A	442	545	3.4e-09	0.15	0.72		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1015	1elw	A	492	572	1e-10	-0.04	0.04		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1015	1elw	A	603	703	3.4e-10	0.27	0.37		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									D;	COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1015	1elw	A	637	737	6.8e-15	0.60	0.90		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1015	1elw	A	660	761	1.1e-15	0.61	1.00		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1015	1elw	A	671	769	1.7e-15	0.41	0.99		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1015	1fch	A	1	109	3.4e-12	0.03	-0.11		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRA TRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1015	1fch	A	290	511	4.4e-19	0.08	1.00		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1015	1fch	A	306	561	8.5e-27	0.27	1.00		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1015	1fch	A	39	360	0.00066	-0.09	0.05		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1015	1fch	A	434	753	2e-23	0.06	0.93		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1015	1fch	A	492	742	1.2e-29	0.25	0.78		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1015	1fch	A	556	766	3.4e-19	0.13	0.25		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1015	1qge	A	593	755	6.6e-06	0.45	0.66		VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	PROTEIN TRANSPORT HELIX-TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT
1020	1ee4	A	136	417	3.6e-09	0.35	0.95		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
1025	1a1h	A	142	224	3.4e-16	-0.20	0.18		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1025	1a1h	A	172	252	1.7e-26	-0.17	0.62		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									SITE; CHAIN: B, C;	FINGER, DNA-BINDING PROTEIN
1025	1a1h	A	396	477	4.4e-45	-0.02	1.00		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1025	1a1h	A	396	478	4.4e-45			79.36	QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1025	1mey	C	171	252	1.7e-43	-0.36	0.93		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1025	1mey	C	199	280	3.4e-47	-0.00	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1025	1mey	C	227	308	3.4e-48	0.35	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1025	1mey	C	227	309	1e-48			102.61	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1025	1mey	C	255	336	1e-48	0.32	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1025	1mey	C	339	420	1e-50	0.32	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1025	1mey	C	367	448	1.7e-50	-0.11	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1025	1mey	C	395	476	3.4e-50	0.09	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1025	1mey	C	423	504	3.4e-38	0.11	0.92		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1025	1mey	C	451	532	8.5e-35	-0.25	0.17		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1025	1tf3	A	424	533	1e-14	-0.44	0.11		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1025	1tf6	A	148	289	3.4e-28	-0.23	0.04		TFIIIA; CHAIN: A, D; 5S	COMPLEX (TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1025	1tf6	A	182	336	2.2e-60	0.00	0.52		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1025	1tf6	A	200	364	2.2e-68	-0.00	0.65		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1025	1tf6	A	256	401	1e-37	0.31	0.99		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1025	1tf6	A	256	420	4.4e-77	0.05	0.90		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1025	1tf6	A	283	445	4.4e-77			112.15	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1025	1tf6	A	284	476	2.2e-76	-0.33	0.21		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1025	1tf6	A	368	514	1.7e-31	-0.28	0.31		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PROTEIN
1025	1tf6	A	368	518	4.4e-56	-0.07	0.21		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1025	1tf6	A	396	543	1e-28	-0.56	0.15		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1025	1ubd	C	160	252	5.1e-27	-0.46	0.28		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1025	1ubd	C	197	308	1.8e-47	-0.27	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1025	1ubd	C	207	308	5.1e-33	-0.24	0.81		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1025	1ubd	C	235	336	1.7e-35	0.00	0.89		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1025	1ubd	C	254	364	1.8e-56	0.38	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1025	1ubd	C	309	420	1.1e-56	0.02	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1025	1ubd	C	319	420	1e-35	-0.05	0.96		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1025	1ubd	C	341	449	1.1e-57			88.16	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1025	1ubd	C	365	476	1.1e-57	-0.35	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1025	1ubd	C	375	476	1.7e-35	0.11	0.88		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1025	1ubd	C	393	504	2.2e-48	-0.31	0.41		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1025	1ubd	C	431	528	1.5e-23	-0.45	0.10		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										REGULATION/DNA)
1025	2gli	A	149	282	5.1e-31	-0.45	0.43		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1025	2gli	A	154	310	2.2e-41	-0.39	0.13		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1025	2gli	A	199	338	1.5e-64	0.10	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1025	2gli	A	227	366	8.8e-73			99.82	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1025	2gli	A	235	363	6.8e-35	0.32	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1025	2gli	A	283	450	8.8e-73	-0.04	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE- FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1025	2gli	A	311	477	4.4e-74	-0.11	0.70		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1025	2gli	A	339	504	2.2e-64	-0.02	0.92		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1025	2gli	A	375	543	8.5e-30	-0.39	0.52		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1030	1a3c		272	341	2.4e-07	-0.06	0.05		PYRIMIDINE OPERON REGULATORY PROTEIN PYRR; CHAIN: NULL;	TRANSCRIPTION REGULATION PYRR; TRANSCRIPTION REGULATION, ATTENUATION PROTEIN, RNA-BINDING 2 PROTEIN, PYRIMIDINE BIOSYNTHESIS, TRANSFERASE, PRASE, 3 PHOSPHORIBOSYLTRANSFE RASE, BIFUNCTIONAL ENZYME
1030	1ao0	A	223	311	0.0048	-0.10	0.05		GLUTAMINE PHOSPHORIBOSYL PYROPHOSPHATE CHAIN: A, B, C, D;	TGLUTAMINE AMIDOTRANSFERASE TRANSFERASE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										GLUTAMINE AMIDOTRANSFERASE, PRTASE, PURINE 2 BIOSYNTHESIS, PHOSPHORIBOSYLTRANSFE RASE, 3 GLYCOSYLTRANSFERASE
1030	1bd3	D	275	337	1.2e-05	0.25	0.25		URACIL PHOSPHORIBOSYLTRANSFERA SE; CHAIN: D, C, B, A;	TRANSFERASE UPRTASE; TRANSFERASE, GLYCOSYLTRANSFERASE, UPRTASE
1030	1cjb	A	272	311	0.00072	-0.55	0.07		HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERA SE; CHAIN: A, B, C, D;	TRANSFERASE MALARIA, PURINE SALVAGE, PHOSPHORIBOSYLTRANSFE RASE, 2 TRANSITION STATE INHIBITOR
1030	1dku	A	38	378	6e-96	0.89	1.00		PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE; CHAIN: A, B;	TRANSFERASE RIBOSE- PHOSPHATE PYROPHOSPHOKINASE; OPEN ALPHA-BETA STRUCTURE, DOMAIN DUPLICATION, 2 PHOSPHORIBOSYLTRANSFE RASE TYPE I FOLD
1030	1opr		145	374	2.4e-29	-0.30	0.18		OROTATE PHOSPHORIBOSYLTRANSFERA SE; 1OPR 4 CHAIN: NULL; 1OPR 5	TRANSFERASE OPRTASE; 1OPR 6
1030	1oro	B	147	378	3.6e-26	-0.32	0.45		OROTATE PHOSPHORIBOSYLTRANSFERA SE; CHAIN: A, B;	PHOSPHORIBOSYLTRANSFE RASE OPRTASE; PYRIMIDINE NUCLEOTIDE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										BIOSYNTHESIS, INHIBITOR-ENZYME 2 COMPLEX, PHOSPHORIBOSYLTRANSFERASE
1033	1a9n	B	303	382	2.2e-18	1.25	1.00		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1033	1b7f	A	160	318	1e-17			81.99	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(P*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*UP*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRANSCRIPTION PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1033	1b7f	A	67	239	1.4e-42	-0.13	0.49		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(P*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*UP*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRANSCRIPTION PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1033	1cvj	A	162	316	3.4e-40			67.97	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN-1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1033	1cvj	A	164	377	8.8e-31	-0.30	0.42		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A	GENE REGULATION/RNA POLY(A) BINDING PROTEIN-1, PABP 1; RRM, PROTEIN-RNA COMPLEX GENE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	REGULATION/RNA
1033	1cvj	A	69	245	3.4e-40	-0.04	0.31		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1033	1cvj	B	162	312	6.6e-31			64.11	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1033	1cvj	B	164	357	3.4e-24	-0.12	0.99		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1033	1cvj	B	164	362	6.6e-31	-0.14	0.17		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1033	1cvj	F	164	299	1.1e-24	0.47	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1033	1cvj	H	164	299	2e-22	0.03	0.78		P, Q, R, S, T; POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN- RNA COMPLEX, GENE REGULATION/RNA
1033	1cvj	H	305	384	1.3e-17	1.37	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP*A P*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN- RNA COMPLEX, GENE REGULATION/RNA
1033	1cx0	A	305	383	2.2e-19	1.14	1.00		U1A PROTEIN; CHAIN: A; HDV RIBOZYME SELF-CLEAVED; CHAIN: B;	RNA BINDING PROTEIN/RNA NESTED DOUBLE PSEUDOKNOT RNA STRUCTURE
1033	1d8z	A	305	379	1.1e-19	1.01	1.00		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1033	1d9a	A	305	376	1.1e-18	0.86	1.00		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1033	1fj7	A	305	378	1.3e-17	0.09	0.17		NUCLEOLIN RBD1; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
1033	1fjc	A	297	378	1.5e-19	0.92	1.00		NUCLEOLIN RBD2; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
1033	1ha1		157	318	1.4e-51			77.02	HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1033	1ha1		162	371	6.8e-24	-0.41	0.48		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1033	1ha1		67	239	1.4e-51	0.04	-0.02		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1033	1osm	A	396	570	8.8e-10	0.89	-0.20		OMP36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE
1033	1pho		410	570	2e-10	0.96	-0.18		OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) 1PHO 3	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1033	1qm9	A	162	374	2.2e-33	-0.24	0.95		POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A;	RIBONUCLEOPROTEIN PTB, PTB-C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION
1033	1qm9	A	305	439	2e-20	0.21	0.15		POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A;	RIBONUCLEOPROTEIN PTB, PTB-C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION
1033	1urn	A	305	378	1.1e-18	0.92	1.00		U1A SPLICEOSOMAL PROTEIN; 1URN 5 CHAIN: A, B, C; 1URN 6 RNA 21MER HAIRPIN (5'-(AP*AP*UP*CP*CP*AP*UP*UP*1URN 11 CHAIN: P, Q, R 1URN 13	COMPLEX (RIBONUCLEOPROTEIN/RNA)
1033	2omf		398	570	2e-12	1.21	-0.17		MATRIX PORIN OUTER MEMBRANE PROTEIN F; 2OMF 5 CHAIN: NULL; 2OMF 6	INTEGRAL MEMBRANE PROTEIN PORIN MATRIX PORIN, OMPF PORIN; 2OMF 7 PORIN, MEMBRANE PROTEIN 2OMF 12
1033	2sxl		305	379	6.6e-20	1.15	1.00		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPLICING
1033	2up1	A	156	327	1.7e-54			76.24	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1;	COMPLEX (RIBONUCLEOPROTEIN/DN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	A) HNRNP A1, UPI; COMPLEX (RIBONUCLEOPROTEIN/DN A), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1033	2up1	A	156	379	6.6e-31	-0.24	0.58		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DN A) HNRNP A1, UPI; COMPLEX (RIBONUCLEOPROTEIN/DN A), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1033	2up1	A	162	374	6.8e-29	-0.34	0.51		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DN A) HNRNP A1, UPI; COMPLEX (RIBONUCLEOPROTEIN/DN A), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1033	2up1	A	67	247	1.7e-54	-0.18	0.21		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DN A) HNRNP A1, UPI; COMPLEX (RIBONUCLEOPROTEIN/DN A), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1033	3sxl	A	161	315	1.8e-31			73.12	SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1033	3sxl	A	162	299	1.8e-31	0.40	1.00		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1033	3sxl	A	242	363	4.4e-23	0.84	1.00		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1033	3sxl	A	67	228	3.4e-41	0.06	0.30		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1034	1chc		13	78	2.2e-12	-0.03	0.77		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
1034	1chc		16	57	5.1e-05	0.14	0.92		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
1034	1fbv	A	18	65	0.0041	0.21	0.89		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
1034	1rmd		1	83	1.1e-11	-0.21	0.39		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1034	1rmd		14	57	0.0031	-0.24	0.82		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
1039	1a9n	A	16	165	4.4e-23	0.62	1.00		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1039	1a9n	A	61	176	8.5e-28	0.50	0.95		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1039	1a9n	C	16	165	4.4e-23	0.79	1.00		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1039	1a9n	C	61	176	8.5e-28	0.23	0.78		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B";	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: B, D;	(NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1039	1d0b	A	10	169	5.1e-19	0.15	0.35		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1039	1d0b	A	4	130	3.4e-25	0.48	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1039	1dce	A	61	157	3.4e-13	0.58	1.00		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 Å 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1039	1ds9	A	8	171	6.8e-29	0.29	0.25		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1039	1fo1	A	72	165	1.7e-21	0.65	0.99		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP, RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1039	1fo1	B	72	165	1.7e-21	0.52	0.99		NUCLEAR RNA EXPORT	RNA BINDING PROTEIN TAP

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									FACTOR 1; CHAIN: A, B;	(NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1040	1a4y	A	29	145	4.4e-10	0.03	0.16		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1040	1a9n	A	16	165	4.4e-23	0.62	1.00		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1040	1a9n	A	61	165	1.2e-24	0.46	0.95		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1040	1a9n	C	16	165	4.4e-23	0.79	1.00		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1040	1a9n	C	61	179	1.7e-25	0.31	0.98		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1040	1d0b	A	28	109	6.6e-14	0.35	0.24		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1040	1d0b	A	29	107	1.1e-12	0.58	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1040	1d0b	A	49	129	1.5e-15	0.59	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1040	1d0b	A	56	138	1.1e-12	0.11	-0.07		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1040	1d0b	A	62	169	6.8e-21	0.27	-0.08		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1040	1dce	A	61	156	1e-15	0.57	1.00		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 Å 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1040	1ds9	A	63	178	1.7e-28	-0.04	0.12		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1040	1fo1	A	72	165	8.5e-21	0.67	0.99		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1040	1fo1	B	72	165	8.5e-21	0.68	1.00		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1040	1fqv	A	26	161	1.3e-08	0.09	0.04		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2- ASSOCIATED PROTEIN P45; CYCLIN A/CDK2- ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1040	1yrg	A	29	130	4.4e-10	-0.09	0.19		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE- ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEMIDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1042	1bkf		181	290	4.8e-25	0.42	0.92		FK506 BINDING PROTEIN; CHAIN: NULL;	ISOMERASE FKBP; ISOMERASE, ROTAMASE
1042	1c9h	A	181	290	9.6e-24	0.15	0.87		FKBP12.6; CHAIN: A;	IMMUNE SYSTEM CALCINEURIN; FKBP12, RAPAMYCIN, COMPLEX, RYANODINE RECEPTOR
1042	1dg3	A	663	863	3.4e-08	0.00	-0.09		INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GUANINE NUCLEOTIDE-BINDING PROTEIN 1; GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, SIGNALING PROTEIN
1042	1dn1	B	663	844	3.6e-11	-0.00	-0.18		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS S NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1042	1qu7	A	636	840	1.2e-09	0.03	-0.13		METHYL-ACCEPTING CHEMOTAXIS PROTEIN I; CHAIN: A, B;	SIGNALING PROTEIN SERINE, CHEMOTAXIS, FOUR HELICAL-BUNDLE
1042	1quu	A	572	798	4.8e-23	0.11	-0.09		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1042	1rot		173	290	3.6e-23	-0.03	1.00		FKBP59-I; CHAIN: NULL;	PROTEIN ROTAMASE (ISOMERASE) FKBP52 OR HSP56; ROTAMASE (ISOMERASE), DOMAIN I (N-TERM) OF A 59 KDA, 2 FK506-BINDING PROTEIN, PEPTIDYL PROLYL CIS-TRANS ISOMERASE
1043	1f3a	A	2	203	2.2e-63	0.84	1.00		GLUTATHIONE S- TRANSFERASE YA CHAIN; CHAIN: A, B;	TRANSFERASE GLUTATHIONE S- TRANSFERASE, GLUTATHIONE
1043	1gsd	A	2	191	1.3e-54			294.58	GLUTATHIONE TRANSFERASE A1-1; 1GSD 5 CHAIN: A, B; 1GSD 6	TRANSFERASE (GLUTATHIONE)
1043	1gsd	A	2	191	1.3e-54	0.86	1.00		GLUTATHIONE TRANSFERASE A1-1; 1GSD 5 CHAIN: A, B; 1GSD 6	TRANSFERASE (GLUTATHIONE)
1043	1gsd	A	2	191	3.4e-50	0.79	1.00		GLUTATHIONE TRANSFERASE A1-1; 1GSD 5 CHAIN: A, B; 1GSD 6	TRANSFERASE (GLUTATHIONE)
1043	1gse	A	2	204	1.2e-55			316.47	GLUTATHIONE TRANSFERASE; 1GSE 6 CHAIN: A, B; 1GSE 7 19	TRANSFERASE (GLUTATHIONE) A1-1 1GSE 19
1043	1gse	A	2	204	1.2e-55	0.88	1.00		GLUTATHIONE TRANSFERASE; 1GSE 6 CHAIN: A, B; 1GSE 7 19	TRANSFERASE (GLUTATHIONE) A1-1 1GSE 19
1044	1f3a	A	2	200	6.6e-63	0.70	1.00		GLUTATHIONE S-	TRANSFERASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									TRANSFERASE YA CHAIN; CHAIN: A, B;	GLUTATHIONE S-TRANSFERASE, GLUTATHIONE
1044	1gsd	A	2	188	5.1e-52			280.52	GLUTATHIONE TRANSFERASE A1-1; 1GSD 5 CHAIN: A, B; 1GSD 6	TRANSFERASE (GLUTATHIONE)
1044	1gsd	A	2	188	5.1e-52	0.55	1.00		GLUTATHIONE TRANSFERASE A1-1; 1GSD 5 CHAIN: A, B; 1GSD 6	TRANSFERASE (GLUTATHIONE)
1044	1gse	A	2	201	6.8e-57			303.78	GLUTATHIONE TRANSFERASE; 1GSE 6 CHAIN: A, B; 1GSE 7	TRANSFERASE (GLUTATHIONE) A1-1 1GSE 19
1044	1gse	A	2	201	6.8e-57	0.75	1.00		GLUTATHIONE TRANSFERASE; 1GSE 6 CHAIN: A, B; 1GSE 7	TRANSFERASE (GLUTATHIONE) A1-1 1GSE 19
1044	1guk	B	5	198	1.1e-57			216.55	GLUTATHIONE S-TRANSFERASE A4-4; CHAIN: A, B;	TRANSFERASE MGSTA4-4, GST5.7; GLUTATHIONE S-TRANSFERASE, GST, CRYSTAL STRUCTURE, 2 OXIDATIVE STRESS, TRANSFERASE
1044	1guk	B	5	198	1.1e-57	0.97	1.00		GLUTATHIONE S-TRANSFERASE A4-4; CHAIN: A, B;	TRANSFERASE MGSTA4-4, GST5.7; GLUTATHIONE S-TRANSFERASE, GST, CRYSTAL STRUCTURE, 2 OXIDATIVE STRESS, TRANSFERASE
1045	1f3a	A	2	203	4.4e-61	0.67	1.00		GLUTATHIONE S-TRANSFERASE YA CHAIN; CHAIN: A, B;	TRANSFERASE GLUTATHIONE S-TRANSFERASE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	.SEQ FOLD score	Compound	PDB annotation
1045	1gsd	A	2	191	1.7e-50			294.85	GLUTATHIONE TRANSFERASE A1-1; 1GSD 5 CHAIN: A, B; 1GSD 6	GLUTATHIONE TRANSFERASE (GLUTATHIONE)
1045	1gsd	A	2	191	1.7e-50	0.72	1.00		GLUTATHIONE TRANSFERASE A1-1; 1GSD 5 CHAIN: A, B; 1GSD 6	TRANSFERASE (GLUTATHIONE)
1045	1gse	A	2	204	6.8e-56			316.48	GLUTATHIONE TRANSFERASE; 1GSE 6 CHAIN: A, B; 1GSE 7	TRANSFERASE (GLUTATHIONE) A1-1 1GSE 19
1045	1gse	A	2	204	6.8e-56	0.68	1.00		GLUTATHIONE TRANSFERASE; 1GSE 6 CHAIN: A, B; 1GSE 7	TRANSFERASE (GLUTATHIONE) A1-1 1GSE 19
1046	1a25	A	599	731	6.8e-29	0.34	0.66		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1046	1byn	A	599	730	1.7e-34	0.49	1.00		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1046	1cun	A	79	286	8.8e-07	0.02	0.55		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	.SEQ FOLD score	Compound	PDB annotation
1046	1dg3	A	68	286	0.0022	-0.47	0.10		INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN
1046	1dqv	A	593	737	1e-26	0.06	0.12		SYNAPTOTAGMIN III; CHAIN: A;	TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1046	1dqv	A	601	764	6.8e-38	0.33	0.83		SYNAPTOTAGMIN III; CHAIN: A;	GUANINE NUCLEOTIDE-BINDING PROTEIN 1; GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, SIGNALING PROTEIN
1046	1dsy	A	598	738	3.4e-30	0.50	0.55		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1046	1rsy		599	727	1.7e-34	0.65	1.00		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) 1RSY 3	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1046	3rpb	A	601	737	1.4e-32	0.47	0.74		RABPHILIN 3-A; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1046	3rpb	A	601	737	1.4e-32	0.47	0.74		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ iFOLD score	Compound	PDB annotation
										ENDOCYTOSIS/EXOCYTOSIS
1054	1a48		1	234	1.7e-60	0.03	0.95		PHOSPHORIBOSYLAMINOIMIDAZOLE-SUCCINOCARBOXAMIDE CHAIN: NULL;	ATP BINDING PROTEIN SAICAR SYNTHETASE; ATP BINDING PROTEIN, CRYSTAL STRUCTURE, 2 PHOSPHORIBOSYLAMINOIMIDAZOLESUCCINOCARBOXAMIDE (SAICAR) 3 SYNTHASE, PURINE BIOSYNTHESIS
1054	1a48		1	240	1.8e-64	0.02	0.89		PHOSPHORIBOSYLAMINOIMIDAZOLE-SUCCINOCARBOXAMIDE CHAIN: NULL;	ATP BINDING PROTEIN SAICAR SYNTHETASE; ATP BINDING PROTEIN, CRYSTAL STRUCTURE, 2 PHOSPHORIBOSYLAMINOIMIDAZOLESUCCINOCARBOXAMIDE (SAICAR) 3 SYNTHASE, PURINE BIOSYNTHESIS
1054	1a48		1	248	1.8e-64			71.32	PHOSPHORIBOSYLAMINOIMIDAZOLE-SUCCINOCARBOXAMIDE CHAIN: NULL;	ATP BINDING PROTEIN SAICAR SYNTHETASE; ATP BINDING PROTEIN, CRYSTAL STRUCTURE, 2 PHOSPHORIBOSYLAMINOIMIDAZOLESUCCINOCARBOXAMIDE (SAICAR) 3 SYNTHASE, PURINE BIOSYNTHESIS
1054	1qcz	A	247	400	5.1e-54	0.47	1.00		N5-	LYASE PURE; THREE-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CARBOXYAMINOIMIDAZOLE RIBONUCLEOTIDE MUTASE; CHAIN: A;	LAYER (ALPHA-BETA-ALPHA) SANDWICH
1058	1bz4	A	3	115	0.0029	-0.41	0.39		APOLIPOPROTEIN E; CHAIN: A;	LIPID BINDING PROTEIN APO-E3; LIPID TRANSPORT, LIPID TRANSPORT, HEPARIN-BINDING, PLASMA 2 PROTEIN, HDL, VLDL REMARK
1058	1dd5	A	102	171	0.00068	-0.04	0.06		RIBOSOME RECYCLING FACTOR; CHAIN: A;	RIBOSOME THREE-HELIX BUNDLE, BETA-ALPHA-BETA SANDWICH, RIBOSOME
1058	1ses	A	38	118	5.1e-06	-0.41	0.11		LIGASE(SYNTHETASE) SERYL-TRNA SYNTHETASE (E.C.6.1.1.11) (SERINE-TRNA LIGASE) 1SES 3 COMPLEXED WITH SERYL-HYDROXAMATE-AMP 1SES 4	
1059	1cun	A	310	511	2.2e-06	0.09	0.03		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1060	1av1	A	1	207	1.3e-05			52.45	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
1060	1cun	A	1	217	1.3e-09			63.27	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1061	1alh	A	439	520	2.2e-40	0.38	1.00		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1061	1alh	A	467	576	2e-35	-0.40	0.21		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1061	1alh	A	495	604	2e-35	-0.21	0.34		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1061	1mey	C	102	183	8.5e-40	-0.04	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	130	211	3.4e-40	0.22	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	158	239	6.8e-41	0.50	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	159	239	1.1e-43	0.49	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	186	267	3.4e-41	0.49	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										(ZINC FINGER/DNA)
1061	1mey	C	186	268	1.8e-46			99.02	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	187	267	1.8e-46	0.61	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	214	295	5.1e-41	0.10	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	214	295	8.8e-43	0.10	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	242	323	6.8e-42	0.62	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	270	351	1.4e-42	0.36	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	271	351	2.2e-44	0.50	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	298	379	1.7e-44	0.41	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	298	379	4.4e-48	0.41	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1061	1mey	C	326	407	2.2e-46	0.30	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	326	407	3.4e-46	0.30	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	354	435	3.4e-47	0.23	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	382	463	6.8e-48	0.16	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	410	491	1.7e-48	0.40	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	438	519	3.4e-49	0.48	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	46	127	3.4e-39	-0.53	0.07		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	466	547	5.1e-50	0.26	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	494	575	5.1e-50	0.49	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	494	603	4.4e-37	0.12	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	522	603	3.4e-50	0.43	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	550	631	1.7e-50	0.33	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	578	659	8.5e-51	0.52	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1061	1mey	C	634	715	3.4e-50	0.39	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	662	743	1.7e-50	0.60	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	690	768	6.8e-47	0.30	0.65		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1mey	C	74	155	6.8e-40	-0.41	0.30		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1061	1tf6	A	103	253	1.5e-32	-0.04	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1061	1tf6	A	103	267	2.2e-66	0.01	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1061	1tf6	A	187	379	2.2e-75	-0.01	0.98		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1061	1tf6	A	215	360	1.7e-32	-0.02	0.99		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1061	1tf6	A	242	407	2.2e-75			103.23	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1061	1tf6	A	327	473	1e-36	0.16	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1061	1tf6	A	355	519	2.2e-68	-0.09	0.98		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1061	1tf6	A	383	528	3.4e-36	0.07	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1061	1tf6	A	495	640	6.8e-37	0.26	1.00		TFIIIA; CHAIN: A, D; 5S	COMPLEX (TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1061	1tf6	A	495	659	1.1e-66	0.24	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1061	1tf6	A	551	715	1.3e-71	-0.04	0.90		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1061	1tf6	A	580	743	6.6e-70	-0.07	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1061	1tf6	A	607	753	1.7e-37	0.26	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1061	1tf6	A	635	767	3.4e-33	0.03	0.74		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1061	1tf6	A	83	239	4.4e-54	-0.14	0.48		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1061	1ubd	C	102	239	1.5e-48	-0.36	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	1ubd	C	159	268	1.1e-51			92.79	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	1ubd	C	163	268	1.1e-51	0.07	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	1ubd	C	240	351	2.2e-52	0.40	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	1ubd	C	269	379	2.2e-54	0.09	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									INITIATOR ELEMENT DNA; CHAIN: A, B;	YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	1ubd	C	301	407	8.5e-31	0.16	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	1ubd	C	324	435	6.6e-51	-0.22	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	1ubd	C	334	435	1e-31	-0.12	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	1ubd	C	352	491	4.4e-49	0.01	0.84		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	1ubd	C	362	463	5.1e-33	0.02	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	1ubd	C	418	519	3.4e-34	0.07	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	1ubd	C	436	575	4.4e-46	0.17	1.00		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	1ubd	C	474	575	3.4e-34	0.15	0.99		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	1ubd	C	492	631	1.5e-46	0.11	0.75		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA- PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	1ubd	C	530	631	5.1e-34	0.31	1.00		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING- YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	1ubd	C	576	687	4.4e-52	0.14	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	1ubd	C	632	744	2e-53	0.19	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	1ubd	C	642	743	3.4e-34	0.26	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1061	1ubd	C	667	767	3.4e-32	0.02	0.25		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	1ubd	C	77	183	1e-27	-0.28	0.78		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	1ubd	C	83	211	4.4e-37	-0.27	0.75		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1061	2gli	A	102	269	1.1e-65	0.05	0.98		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1061	2gli	A	187	353	4.4e-68	0.40	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	BINDING PROTEIN/DNA)
1061	2gli	A	270	409	3.4e-31	0.24	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1061	2gli	A	271	409	2e-68	0.42	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1061	2gli	A	326	462	1.7e-31	0.14	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1061	2gli	A	326	521	1.1e-67	0.09	0.88		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1061	2gli	A	354	577	2.2e-63	0.00	0.52		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1061	2gli	A	418	546	3.4e-33	0.24	0.95		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1061	2gli	A	494	661	2.2e-65	-0.07	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1061	2gli	A	502	630	1e-33	0.46	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1061	2gli	A	550	716	2.2e-67	0.06	0.68		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1061	2gli	A	606	745	6.6e-68			90.74	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1061	2gli	A	606	745	6.6e-68	0.35	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1061	2gli	A	614	745	1.2e-34	0.46	1.00		ZINC FINGER PROTEIN GLI1;	COMPLEX (DNA-BINDING PROTEIN/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A; DNA; CHAIN: C, D;	PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1061	2gli	A	642	767	1.2e-32	0.07	0.48		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1061	2gli	A	74	213	1.7e-27	-0.13	0.30		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1064	1alh	A	107	185	5.1e-20	0.12	-0.18		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1064	1mey	C	106	186	3.4e-33	-0.29	0.13		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	135	212	6.8e-36	-0.26	0.24		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	163	240	1.7e-36	0.09	0.86		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	187	268	6.8e-42	0.38	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	187	296	6.6e-42	-0.33	0.15		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	215	296	5.1e-44	0.09	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1064	1mey	C	215	324	8.8e-42	0.08	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	243	324	5.1e-45	0.35	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	271	352	1.5e-45	0.26	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	272	352	8.8e-46	0.27	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	299	380	5.1e-46	0.07	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	327	408	1e-46	0.15	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	355	436	5.1e-47	0.14	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	383	464	8.5e-47	0.59	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	411	492	3.4e-47	0.60	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1064	1mey	C	439	520	1.7e-48	0.57	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	467	548	3.4e-49	0.57	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	495	576	1e-49	0.62	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	523	604	3.4e-50	0.34	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	551	632	1.4e-50	0.61	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	551	633	1e-50			103.75	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	579	660	1e-50	0.66	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	635	716	1e-50	0.35	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	663	744	1.7e-50	0.28	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	691	772	1.7e-50	0.36	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	C	719	785	1.7e-40	0.05	0.93		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1mey	G	185	212	5.1e-09	-0.14	0.42		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1064	1tf6	A	188	338	3.4e-34	0.08	0.96		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1064	1tf6	A	188	352	6.6e-69	-0.07	0.82		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1064	1tf6	A	272	417	3.4e-34	-0.12	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1064	1tf6	A	272	436	1.1e-72	-0.05	0.99		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1064	1tf6	A	328	473	3.4e-35	-0.18	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1064	1tf6	A	356	501	3.4e-36	0.12	0.99		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1064	1tf6	A	412	576	4.4e-71	-0.12	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1064	1tf6	A	468	613	6.8e-37	0.42	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1064	1tf6	A	468	632	2.2e-73	0.06	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										INITIATION, ZINC FINGER PROTEIN
1064	1tf6	A	552	716	2.2e-73	0.01	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1064	1tf6	A	579	742	2.2e-73			108.49	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1064	1tf6	A	580	725	6.8e-38	0.25	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1064	1tf6	A	608	772	2.2e-71	0.11	0.96		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1064	1tf6	A	636	785	3.4e-37	0.27	0.96		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1064	1ubd	C	112	212	5.1e-24	-0.45	0.11		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1064	1ubd	C	166	268	3.4e-28	0.12	0.75		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1064	1ubd	C	195	296	6.8e-31	-0.19	0.94		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									INITIATOR ELEMENT DNA; CHAIN: A, B;	YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1064	1ubd	C	248	353	4.4e-52	0.07	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1064	1ubd	C	269	381	4.4e-55	0.02	0.98		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1064	1ubd	C	297	408	4.4e-51	-0.00	0.98		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1064	1ubd	C	382	492	1.8e-49	0.27	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1064	1ubd	C	409	520	2.2e-52	0.08	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1064	1ubd	C	447	548	5.1e-34	0.29	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1064	1ubd	C	465	577	2.2e-56	0.10	1.00		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1064	1ubd	C	497	604	6.8e-35	0.24	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1064	1ubd	C	521	632	1.1e-56	0.31	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1064	1ubd	C	578	689	1.3e-54	0.22	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1064	1ubd	C	579	689	1.3e-54			94.34	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1064	1ubd	C	605	745	1.3e-52	0.06	0.88		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1064	1ubd	C	615	716	1.7e-34	0.35	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1064	1ubd	C	640	744	3.4e-35	-0.05	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1064	1ubd	C	661	772	8.8e-52	0.08	0.98		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1064	1ubd	C	671	772	1.7e-34	0.01	0.96		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1064	2gli	A	114	242	1.7e-23	-0.25	0.10		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										BINDING PROTEIN/DNA)
1064	2gli	A	135	267	5.1e-27	-0.18	0.58		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1064	2gli	A	166	326	2.2e-54	-0.17	0.66		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1064	2gli	A	187	354	8.8e-69	-0.03	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1064	2gli	A	272	409	1.1e-66	0.31	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1064	2gli	A	356	522	1.1e-67	0.05	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1064	2gli	A	383	550	1.1e-66	0.13	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1064	2gli	A	411	578	1.1e-69	0.31	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1064	2gli	A	467	606	4.4e-71	0.50	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1064	2gli	A	523	662	4.4e-71			96.67	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1064	2gli	A	551	690	6.6e-70	0.44	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1064	2gli	A	607	774	6.6e-70	0.13	0.96		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1064	2gli	A	643	771	6.8e-34	0.26	0.86		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1065	1bw6	A	17	62	6.8e-10	-0.32	0.63		CENTROMERE PROTEIN B; CHAIN: A;	DNA BINDING PROTEIN CENTROMERE PROTEIN, DNA-BINDING, HELIX-TURN-HELIX, DNA 2 BINDING PROTEIN
1074	1a60		17	183	9.6e-58	-0.02	0.99		PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE
1074	1aq1		1	197	7.2e-57			92.78	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1074	1aq1		18	183	7.2e-57	0.20	0.99		CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1074	1bi8	A	17	183	2.4e-62	0.27	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1074	1bi8	A	3	183	2.4e-62			92.60	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1074	1cm8	A	17	183	4.8e-58	0.52	1.00		PHOSPHORYLATED MAP KINASE P38-GAMMA; CHAIN: A, B;	TRANSFERASE STRESS-ACTIVATED PROTEIN KINASE-3, ERK6, ERK5; P38-GAMMA, GAMMA, PHOSPHORYLATION, MAP KINASE
1074	1hcl		1	197	1.2e-61			102.19	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1074	1hcl		18	183	1.2e-61	0.30	1.00		HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1074	1ian		18	172	3.6e-44	-0.06	0.99		P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
1074	1p38		18	172	1.2e-54	0.10	1.00		MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1074	3erk		1	236	4.8e-62			80.11	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1074	3erk		18	183	4.8e-62	0.18	1.00		EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1093	1ais	B	203	371	1.2e-21	0.10	0.15		TATA-BINDING PROTEIN;	COMPLEX (RIBOSOME

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: A; TRANSCRIPTION INITIATION FACTOR IIB; CHAIN: B; DNA; CHAIN: C, E;	BINDING/DNA) TBP; TFB TFIIB; TRANSCRIPTION, HYPERTHERMOPHILE, RIBOSOME BINDING, 2 COMPLEX (RIBOSOME BINDING/DNA)
1093	1ais	B	283	383	0.0041	0.22	0.09		TATA-BINDING PROTEIN; CHAIN: A; TRANSCRIPTION INITIATION FACTOR IIB; CHAIN: B; DNA; CHAIN: C, E;	COMPLEX (RIBOSOME BINDING/DNA) TBP; TFB TFIIB; TRANSCRIPTION, HYPERTHERMOPHILE, RIBOSOME BINDING, 2 COMPLEX (RIBOSOME BINDING/DNA)
1093	1bu2	A	148	374	3.4e-32	0.57	1.00		CYCLIN HOMOLOG; CHAIN: A;	CELL CYCLE REGULATION, CELL CYCLE REGULATION, HERPESVIRUS SAIMIRI, VIRAL CYCLIN
1093	1bu2	A	148	376	1e-56			142.44	CYCLIN HOMOLOG; CHAIN: A;	CELL CYCLE REGULATION, CELL CYCLE REGULATION, HERPESVIRUS SAIMIRI, VIRAL CYCLIN
1093	1bu2	A	162	369	1e-56	0.30	1.00		CYCLIN HOMOLOG; CHAIN: A;	CELL CYCLE REGULATION, CELL CYCLE REGULATION, HERPESVIRUS SAIMIRI, VIRAL CYCLIN
1093	1c9b	A	203	392	1e-25	0.31	0.82		GENERAL TRANSCRIPTION FACTOR IIB; CHAIN: A, E, I, M, Q; TATA BOX BINDING PROTEIN; CHAIN: B, F, J, N, R; ADMLP TATA-BOX DNA CONTAINING IIB RECOGNITION	TRANSCRIPTION/DNA TRANSCRIPTION INITIATION FACTOR IIB, TFIIB; TATA-BOX FACTOR, TATA SEQUENCE-BINDING PROTEIN, PROTEIN-DNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									CHAIN: C, G, K, O, S; ADMPLP TATA-BOX DNA CONTAINING IIB RECOGNITION CHAIN: D, H, L, P, T;	COMPLEX, CYCLIN-LIKE FOLD, HELIX-TURN-HELIX, 2 TATA-BOX, TRANSCRIPTION/DNA
1093	1jkw		132	405	1.6e-37			80.49	CYCLIN H; CHAIN: NULL;	CELL DIVISION RCYCLIN H (RECOMBINANT); CYCLIN, CELL CYCLE, CELL DIVISION, NUCLEAR PROTEIN
1093	1jkw		153	370	1.6e-37	0.10	1.00		CYCLIN H; CHAIN: NULL;	CELL DIVISION RCYCLIN H (RECOMBINANT); CYCLIN, CELL CYCLE, CELL DIVISION, NUCLEAR PROTEIN
1093	1jkw		202	388	1.2e-24	-0.04	0.54		CYCLIN H; CHAIN: NULL;	CELL DIVISION RCYCLIN H (RECOMBINANT); CYCLIN, CELL CYCLE, CELL DIVISION, NUCLEAR PROTEIN
1093	1qmz	B	142	389	1.7e-62	0.58	1.00		CELL DIVISION PROTEIN KINASE 2; CHAIN: A, C; G2/MITOTIC-SPECIFIC CYCLIN A; CHAIN: B, D; SUBSTRATE PEPTIDE; CHAIN: E, F;	COMPLEX (PROTEIN KINASE/CYCLIN) CYCLIN-DEPENDENT KINASE-2, CDK2, P33 PROTEIN KINASE; CCNA, CCN1; COMPLEX (PROTEIN KINASE/CYCLIN), CYCLIN, CDK, 2 PHOSPHORYLATION, SUBSTRATE COMPLEX
1093	1vin		148	389	5.1e-62	0.65	1.00		CYCLIN A; CHAIN: NULL;	BINDING PROTEIN CYCLIN, CELL CYCLE, KINASE-REGULATORY-SUBUNIT, 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1093	1vin		148	406	5.1e-62			141.42	CYCLIN A; CHAIN: NULL;	BINDING PROTEIN BINDING PROTEIN CYCLIN, CELL CYCLE, KINASE-REGULATORY-SUBUNIT, 2 BINDING PROTEIN
1095	1a26		1027	1155	1.8e-09	0.20	0.12		POLY (ADP-RIBOSE) POLYMERASE; CHAIN: NULL;	TRANSFERASE PARP-CF, POLY(ADP-RIBOSE) TRANSFERASE, POLY TRANSFERASE, GLYCOSYLTRANSFERASE, NAD(+) 2 ADP-RIBOSYLTRANSFERASE
1103	1a25	A	158	245	8.4e-13	0.06	0.92		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1103	1a25	A	26	149	3.6e-16	0.45	1.00		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1103	1dix	A	172	245	3.6e-07	-0.35	0.48		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1103	1dix	A	39	162	9.6e-13	-0.11	0.98		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, 2 LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1103	1dix	B	172	245	6e-07	-0.59	0.09		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, 2 LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1103	1dix	B	39	162	1.2e-12	0.09	0.94		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, 2 LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1103	1dsy	A	158	245	2.4e-12	0.06	0.90		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM ⁺⁺ , PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PHOSPHATIDYL SERINE, PROTEIN KINASE C
1103	1dsy	A	26	147	2.4e-16	0.38	1.00		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM ⁺⁺ , PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1103	3rpb	A	158	245	9.6e-12	0.42	0.96		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS S
1103	3rpb	A	27	166	9.6e-16	0.28	0.49		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS S
1115	1bbo		102	128	0.00072	-0.82	0.05		DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 11 1BBO 3 REPLACED BY ABU (C11ABU) (NMR, 60 STRUCTURES) 1BBO 4	
1115	1mey	C	102	128	0.0012	-0.82	0.25		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1115	1mey	C	108	217	9.6e-15	-0.62	0.13		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1115	1mey	C	163	245	3.6e-28	-0.44	0.74		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1115	1mey	C	196	273	4.8e-39	0.34	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1115	1mey	C	220	301	3.6e-38	0.00	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1115	1mey	C	248	329	1.2e-37	-0.39	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1115	1mey	C	276	357	2.4e-38	0.47	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1115	1mey	C	305	385	2.4e-40	0.59	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1115	1mey	C	332	413	3.6e-43	0.27	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1115	1mey	C	360	441	4.8e-44	0.34	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1115	1mey	C	360	442	6e-45			109.61	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1115	1mey	C	388	469	6e-45	0.34	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1115	1mey	C	416	497	1.1e-43	0.38	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1115	1tf6	A	196	357	1.2e-61	0.00	0.81		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1115	1tf6	A	221	385	1.2e-61	0.27	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1115	1tf6	A	332	497	6e-71			120.92	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1115	1tf6	A	333	497	6e-71	0.05	0.83		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1115	1ubd	C	175	273	4.8e-40	-0.21	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-FINGER RECOGNITION, 3

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
1115	1ubd	C	197	301	3.6e-46	-0.14	0.92		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA)
1115	1ubd	C	218	357	3.6e-47	-0.09	0.58		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1115	1ubd	C	303	413	1.2e-50	0.03	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1115	1ubd	C	359	469	3.6e-53	-0.03	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-REGULATION/DNA) YING-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
									INITIATOR ELEMENT DNA; CHAIN: A, B;	YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1115	1ubd	C	386	497	1.2e-53	-0.10	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1115	1ubd	C	388	498	1.2e-53			105.73	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1115	1ubd	C	94	217	7.2e-13	-0.78	0.05		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQ FOLD score	Compound	PDB annotation
										PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1115	2gli	A	137	274	1.2e-42	-0.19	0.74		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1115	2gli	A	196	331	3.6e-56	0.41	0.98		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1115	2gli	A	248	415	1.2e-62	0.18	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1115	2gli	A	304	443	7.2e-68			107.13	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1115	2gli	A	305	443	2.4e-66	0.41	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1115	2gli	A	332	471	7.2e-68	0.24	0.93		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC